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Byrne, Michael P.
Middlebrook, John L.
Lapenotiere, Hugh
Clayton, Michael A.
Brown, Douglas R.

<120> RECOMBINANT VACCINE AGAINST BOTULINUM
NEUROTOXIN

<130> A33626-A 067252.0107

<140> 09/611,419

<141> 2000-07-06

<150> PCT/US00/12890

<151> 2000-05-12

<150> 60/133,865

<151> 1999-05-12

<150> 60/133,866

<151> 1999-05-12

<150> 60/133,867

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ga <150> 60/133,868

<151> 1999-05-12

<150> 60/133,869

<151> 1999-05-12

<150> 60/146,192

<151> 1999-07-29

<160> 42

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1332

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hc

<221> CDS

<222> (13)...(1326)

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Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn

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10

atc atc aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg 99

Ile	Ile	Asn	Thr	Ser	Ile	Leu	Asn	Leu	Arg	Tyr	Glu	Ser	Asn	His	Leu	
15						20					25					
atc	gac	ctg	tct	cgc	tac	gct	tcc	aaa	atc	aac	atc	ggg	tct	aaa	gtt	147
Ile	Asp	Leu	Ser	Arg	Tyr	Ala	Ser	Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	
30					35					40					45	
aac	ttc	gat	ccg	atc	gac	aag	aat	cag	atc	cag	ctg	ttc	aat	ctg	gaa	195
Asn	Phe	Asp	Pro	Ile	Asp	Lys	Asn	Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	
				50					55					60		
tct	tcc	aaa	atc	gaa	gtt	atc	ctg	aag	aat	gct	atc	gta	tac	aac	tct	243
Ser	Ser	Lys	Ile	Glu	Val	Ile	Leu	Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	
			65					70					75			
atg	tac	gaa	aac	ttc	tcc	acc	tcc	ttc	tgg	atc	cgt	atc	ccg	aaa	tac	291
Met	Tyr	Glu	Asn	Phe	Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	
		80					85					90				
ttc	aac	tcc	atc	tct	ctg	aac	aat	gaa	tac	acc	atc	atc	aac	tgc	atg	339
Phe	Asn	Ser	Ile	Ser	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	
	95					100					105					
gaa	aac	aat	tct	ggg	tgg	aaa	gta	tct	ctg	aac	tac	ggg	gaa	atc	atc	387
Glu	Asn	Asn	Ser	Gly	Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	
110					115					120					125	
tgg	act	ctg	cag	gac	act	cag	gaa	atc	aaa	cag	cgt	gtt	gta	ttc	aaa	435
Trp	Thr	Leu	Gln	Asp	Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	
				130					135					140		
tac	tct	cag	atg	atc	aac	atc	tct	gac	tac	atc	aat	cgc	tgg	atc	ttc	483
Tyr	Ser	Gln	Met	Ile	Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	
			145					150					155			
gtt	acc	atc	acc	aac	aat	cgt	ctg	aat	aac	tcc	aaa	atc	tac	atc	aac	531
Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	
		160					165					170				
ggc	cgt	ctg	atc	gac	cag	aaa	ccg	atc	tcc	aat	ctg	ggg	aac	atc	cac	579
Gly	Arg	Leu	Ile	Asp	Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	
	175					180					185					
gct	tct	aat	aac	atc	atg	ttc	aaa	ctg	gac	ggg	tgt	cgt	gac	act	cac	627
Ala	Ser	Asn	Asn	Ile	Met	Phe	Lys	Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	
190					195					200					205	
cgc	tac	atc	tgg	atc	aaa	tac	ttc	aat	ctg	ttc	gac	aaa	gaa	ctg	aac	675
Arg	Tyr	Ile	Trp	Ile	Lys	Tyr	Phe	Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	
				210					215					220		
gaa	aaa	gaa	atc	aaa	gac	ctg	tac	gac	aac	cag	tcc	aat	tct	ggg	atc	723
Glu	Lys	Glu	Ile	Lys	Asp	Leu	Tyr	Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	
			225					230						235		
ctg	aaa	gac	ttc	tgg	ggg	gac	tac	ctg	cag	tac	gac	aaa	ccg	tac	tac	771
Leu	Lys	Asp	Phe	Trp	Gly	Asp	Tyr	Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	

CG

240	245	250	
atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val 255 260 265			819
ggg atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met 270 275 280 285			867
act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe 290 295 300			915
atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn 305 310 315			963
aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg 320 325 330			1011
ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala 335 340 345			1059
ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys 350 355 360 365			1107
tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln 370 375 380			1155
gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn 385 390 395			1203
aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu 400 405 410			1251
cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp 415 420 425			1299
gac ggt tgg ggt gaa cgt ccg ctg taa gaattc Asp Gly Trp Gly Glu Arg Pro Leu * 430 435			1332

<210> 2

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hc

<400> 2

Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn
1 5 10 15
Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
20 25 30
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
35 40 45
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
50 55 60
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
65 70 75 80
Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
85 90 95
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
100 105 110
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
115 120 125
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
130 135 140
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
145 150 155 160
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
165 170 175
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
180 185 190
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
195 200 205
Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
210 215 220
Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
225 230 235 240
Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
245 250 255
Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
260 265 270
Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
275 280 285
Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
290 295 300
Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
305 310 315 320
Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
325 330 335
Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
340 345 350
Pro Asp Val Gly Asn Leu Ser Gln Val Val Met Lys Ser Lys Asn
355 360 365
Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
370 375 380
Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
385 390 395 400
Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
405 410 415
Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp

420
Gly Glu Arg Pro Leu
435

425

430

<210> 3
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<213> Artificial Sequence

<220>
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<221> CDS
<222> (13)...(1314)

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acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac ctg 99
Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
15 20 25

tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc gat 147
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
30 35 40 45

ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc aaa 195
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
50 55 60

atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac gaa 243
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
65 70 75

aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac tcc 291
Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
80 85 90

atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac aat 339
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
95 100 105

tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act ctg 387
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
110 115 120 125

cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct cag 435
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
130 135 140

atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc atc 483
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
145 150 155

acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt ctg 531
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
160 165 170

atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct aat 579
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
175 180 185

aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac atc 627
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
190 195 200 205

tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa gaa 675
Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
210 215 220

atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa gac 723
Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
225 230 235

ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg aat 771
Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
240 245 250

ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc cgc 819
Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
255 260 265

ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc aac 867
Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
270 275 280 285

atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc atc atc aag 915
Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
290 295 300

aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac aat gat cgt 963
Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
305 310 315

gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt ctg gct acc 1011
Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
320 325 330

aat gct tct cag gct ggt gta gaa aag atc ttg tct gct ctg gaa atc 1059
Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
335 340 345

ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa tcc aag aac 1107
Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
350 355 360 365

gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag gac aac aat 1155
Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
370 375 380

ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac aat atc gct 1203

Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
 385 390 395

aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa cgt tcc tct 1251
 Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
 400 405 410

cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat gac ggt tgg 1299
 Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp
 415 420 425

ggt gaa cgt ccg ctg taagaattc 1323
 Gly Glu Arg Pro Leu
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<210> 4

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
 on BoNTA Hc

<400> 4

Met Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile
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 Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp
 35 40 45
 Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val
 50 55 60
 Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser
 65 70 75 80
 Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu
 85 90 95
 Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp
 100 105 110
 Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr
 115 120 125
 Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn
 130 135 140
 Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn
 145 150 155 160
 Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
 165 170 175
 Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met
 180 185 190
 Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys
 195 200 205
 Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp
 210 215 220
 Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly
 225 230 235 240
 Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp

65	70	75	
gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac	291		
Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn			
80 85 90			
tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac	339		
Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn			
95 100 105			
aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act	387		
Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr			
110 115 120 125			
ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct	435		
Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser			
130 135 140			
cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc	483		
Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr			
145 150 155			
atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt	531		
Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg			
160 165 170			
ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct	579		
Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser			
175 180 185			
aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac	627		
Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr			
190 195 200 205			
atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa	675		
Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys			
210 215 220			
gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa	723		
Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys			
225 230 235			
gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg	771		
Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu			
240 245 250			
aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc	819		
Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile			
255 260 265			
cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc	867		
Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr			
270 275 280 285			
aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc atc atc	915		
Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile			
290 295 300			

69

aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac aat gat 963
Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp
305 310 315

cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt ctg gct 1011
Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala
320 325 330

acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct ctg gaa 1059
Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu
335 340 345

atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa tcc aag 1107
Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys
350 355 360 365

aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag gac aac 1155
Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn
370 375 380

aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac aat atc 1203
Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile
385 390 395

gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa cgt tcc 1251
Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser
400 405 410

tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat gac ggt 1299
Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly
415 420 425

Ca tgg ggt gaa cgt ccg ctg taagaattc 1326
Trp Gly Glu Arg Pro Leu
430 435

<210> 6

<211> 435

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hc

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Met Ala Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser
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Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg
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Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile
35 40 45
Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu
50 55 60
Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe

65 70 75 80
 Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser
 85 90 95
 Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly
 100 105 110
 Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp
 115 120 125
 Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile
 130 135 140
 Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn
 145 150 155 160
 Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp
 165 170 175
 Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile
 180 185 190
 Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile
 195 200 205
 Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys
 210 215 220
 Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp
 225 230 235 240
 Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr
 245 250 255
 Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr
 260 265 270
 Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr
 275 280 285
 Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr
 290 295 300
 Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr
 305 310 315 320
 Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala
 325 330 335
 Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp
 340 345 350
 Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln
 355 360 365
 Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn
 370 375 380
 Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu
 385 390 395 400
 Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr
 405 410 415
 Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
 420 425 430
 Arg Pro Leu
 435

<210> 7

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hc

<221> CDS

<222> (10)...(1329)

<400> 7

gaattcacg atg gcc aac aaa tac aat tcc gaa atc ctg aac aat atc atc 51

Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile

1

5

10

ctg aac ctg cgt tac aaa gac aac aat ctg atc gat ctg tct ggt tac 99

Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr

15

20

25

30

ggt gct aaa gtt gaa gta tac gac ggt gtt gaa ctg aat gac aag aac 147

Gly Ala Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn

35

40

45

cag ttc aaa ctg acc tct tcc gct aac tct aag atc cgt gtt act cag 195

Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln

50

55

60

aat cag aac atc atc ttc aac tcc gta ttc ctg gac ttc tct gtt tcc 243

Asn Gln Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser

65

70

75

ttc tgg atc cgt atc ccg aaa tac aag aac gac ggt atc cag aat tac 291

Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr

80

85

90

atc cac aat gaa tac acc atc atc aac tgc atg aag aat aac tct ggt 339

Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly

95

100

105

110

tggt aag atc tcc atc cgc ggt aac cgt atc atc tgg act ctg atc gat 387

Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp

115

120

125

atc aac ggt aag acc aaa tct gta ttc ttc gaa tac aac atc cgt gaa 435

Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu

130

135

140

gac atc tct gaa tac atc aat cgc tgg ttc ttc gtt acc atc acc aat 483

Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn

145

150

155

aac ctg aac aat gct aaa atc tac atc aac ggt aaa ctg gaa tct aat 531

Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn

160

165

170

acc gac atc aaa gac atc cgt gaa gtt atc gct aac ggt gaa atc atc 579

Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile

175

180

185

190

ttc aaa ctg gac ggt gac atc gat cgt acc cag ttc atc tgg atg aaa 627

Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys

195

200

205

tac ttc tcc atc ttc aac acc gaa ctg tct cag tcc aat atc gaa gaa 675

Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu	
210 215 220	
cgg tac aag atc cag tct tac tcc gaa tac ctg aaa gac ttc tgg ggt	723
Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly	
225 230 235	
aat ccg ctg atg tac aac aaa gaa tac tat atg ttc aat gct ggt aac	771
Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn	
240 245 250	
aag aac tct tac atc aaa ctg aag aaa gac tct ccg gtt ggt gaa atc	819
Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile	
255 260 265 270	
ctg act cgt tcc aaa tac aac cag aac tct aaa tac atc aac tac cgc	867
Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg	
275 280 285	
gac ctg tac atc ggt gaa aag ttc atc atc cgt cgc aaa tct aac tct	915
Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser	
290 295 300	
cag tcc atc aat gat gac atc gta cgt aaa gaa gac tac atc tac ctg	963
Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu	
305 310 315	
gac ttc ttc aac ctg aat cag gaa tgg cgt gta tac acc tac aag tac	1011
Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr	
320 325 330	
ttc aag aaa gaa gaa gaa aag ctt ttc ctg gct ccg atc tct gat tcc	1059
Phe Lys Lys Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser	
335 340 345 350	
gac gaa ctc tac aac acc atc cag atc aaa gaa tac gac gaa cag ccg	1107
Asp Glu Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro	
355 360 365	
acc tac tct tgc cag ctg ctg ttc aag aaa gat gaa gaa tct act gac	1155
Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp	
370 375 380	
gaa atc ggt ctg atc ggt atc cac cgt ttc tac gaa tct ggt atc gta	1203
Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val	
385 390 395	
ttc gaa gaa tac aaa gac tac ttc tgc atc tcc aaa tgg tac ctg aag	1251
Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys	
400 405 410	
gaa gtt aaa cgc aaa ccg tac aac ctg aaa ctg ggt tgc aat tgg cag	1299
Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln	
415 420 425 430	
ttc atc ccg aaa gac gaa ggt tgg acc gaa tagtaagaat tc	1341
Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu	

<210> 8

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTB Hc

<400> 8

Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn
 1 5 10 15
 Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala
 20 25 30
 Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe
 35 40 45
 Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln
 50 55 60
 Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp
 65 70 75 80
 Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His
 85 90 95
 Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys
 100 105 110
 Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn
 115 120 125
 Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile
 130 135 140
 Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu
 145 150 155 160
 Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp
 165 170 175
 Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys
 180 185 190
 Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe
 195 200 205
 Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr
 210 215 220
 Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro
 225 230 235 240
 Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn
 245 250 255
 Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr
 260 265 270
 Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu
 275 280 285
 Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser
 290 295 300
 Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe
 305 310 315 320
 Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys
 325 330 335
 Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu
 340 345 350

Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr
 355 360 365
 Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile
 370 375 380
 Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu
 385 390 395 400
 Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val
 405 410 415
 Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile
 420 425 430
 Pro Lys Asp Glu Gly Trp Thr Glu
 435 440

<210> 9

<211> 1371

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hc

<221> CDS

<222> (10)...(1359)

<400> 9


gaattcacg atg acc atc cca ttc aac atc ttc tcc tac acc aac aac tcc 51
 Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser

1

5

10

ctg ttg aag gac atc atc aac gag tac ttc aac aac atc aac gac tcc 99
 Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser
 15 20 25 30


 aag atc ctg tcc ctg cag aac cgt aag aac acc ttg gtc gac acc tcc 147
 Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser
 35 40 45

ggt tac aac gcc gag gtc tcc gag gag ggt gac gtc cag ctg aac cca 195
 Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro
 50 55 60

atc ttc cca ttc gac ttc aag ctg ggt tcc tcc ggt gag gac aga ggt 243
 Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly
 65 70 75

aag gtc atc gtc acc cag aac gag aac atc gtc tac aac tcc atg tac 291
 Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr
 80 85 90

gag tcc ttc tcc atc tcc ttc tgg atc aga atc aac aag tgg gtc tcc 339
 Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser
 95 100 105 110

aac ttg cca ggt tac acc atc atc gac tcc gtc aag aac aac tcc ggt 387
 Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly
 115 120 125

tgg tcc atc ggt atc atc tcc aac ttc ctg gtc ttc acc ctg aag cag	435
Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln	
130 135 140	

aac gag gac tcc gag cag tcc atc aac ttc tcc tac gac atc tcc aac	483
Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn	
145 150 155	

aac gct cct ggt tac aac aag tgg ttc ttc gtc acc gtc acc aac aac	531
Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn	
160 165 170	

atg atg ggt aac atg aag atc tac atc aac ggt aag ctg atc gac acc	579
Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr	
175 180 185 190	

atc aag gtc aag gag ttg acc ggt atc aac ttc tcc aag acc atc acc	627
Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr	
195 200 205	

ttc gag atc aac aag atc cca gac acc ggt ctg atc acc tcc gac tcc	675
Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser	
210 215 220	

gac aac atc aac atg tgg atc cgt gac ttc tac atc ttc gcc aag gag	723
Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu	
225 230 235	

ttg gac ggt aag gac atc aac atc ctg ttc aac tcc ttg cag tac acc	771
Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr	
240 245 250	

aac gtc gtc aag gac tac tgg ggt aac gac ctg aga tac aac aag gag	819
Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu	
255 260 265 270	

tac tac atg gtc aac atc gac tac ttg aac aga tac atg tac gcc aac	867
Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn	
275 280 285	

tcc aga cag atc gtc ttc aac acc aga cgt aac aac aac gac ttc aac	915
Ser Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn	
290 295 300	

gag ggt tac aag atc atc atc aag cgt atc aga ggt aac acc aac gac	963
Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp	
305 310 315	

acc aga gtc aga ggt ggt gac atc ctg tac ttc gac atg act atc aac	1011
Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn	
320 325 330	

aac aag gcc tac aac ctg ttc atg aag aac gag acc atg tac gcc gac	1059
Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp	
335 340 345 350	

aac cac tcc acc gag gac atc tac gcc atc ggt ctg cgt gag cag acc 1107
 Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr
 355 360 365
 aag gac atc aac gac aac atc atc ttc cag atc cag cca atg aac aac 1155
 Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn
 370 375 380
 act tac tac tac gct tcc cag atc ttc aag tcc aac ttc aac ggt gag 1203
 Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu
 385 390 395
 aac atc tcc ggt atc tgt tcc atc ggt acc tac aga ttc cgt ctg ggt 1251
 Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly
 400 405 410
 ggt gac tgg tac aga cac aac tac ttg gtt cca act gtc aag cag ggt 1299
 Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly
 415 420 425 430
 aac tac gcc tcc ttg ctg gag tcc act tcc acc cac tgg gga ttc gtc 1347
 Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val
 435 440 445
 cca gtc tcc gag taataggaat tc 1371
 Pro Val Ser Glu
 450

<210> 10

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTC Hc

<400> 10

Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu
 1 5 10 15
 Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser Lys Ile
 20 25 30
 Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser Gly Tyr
 35 40 45
 Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro Ile Phe
 50 55 60
 Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly Lys Val
 65 70 75 80
 Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr Glu Ser
 85 90 95
 Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser Asn Leu
 100 105 110
 Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly Trp Ser
 115 120 125
 Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln Asn Glu
 130 135 140

Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn Asn Ala
 145 150 155 160
 Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn Met Met
 165 170 175
 Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr Ile Lys
 180 185 190
 Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr Phe Glu
 195 200 205
 Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser Asp Asn
 210 215 220
 Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu Leu Asp
 225 230 235 240
 Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr Asn Val
 245 250 255
 Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr
 260 265 270
 Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn Ser Arg
 275 280 285
 Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn Glu Gly
 290 295 300
 Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp Thr Arg
 305 310 315 320
 Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn Asn Lys
 325 330 335
 Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp Asn His
 340 345 350
 Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr Lys Asp
 355 360 365
 Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn Thr Tyr
 370 375 380
 Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu Asn Ile
 385 390 395 400
 Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly Gly Asp
 405 410 415
 Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly Asn Tyr
 420 425 430
 Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val Pro Val
 435 440 445
 Ser Glu
 450

<210> 11
 <211> 1374
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (10)...(1362)

<400> 11
 gaattcacg atg cgt ttg aag gct aag gtc aac gag tcc ttc gag aac acc 51
 Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr
 1 5 10

atg cca ttc aac atc ttc tcc tac acc aac aac tcc ttg ttg aag gac	99
Met Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp	
15 20 25 30	
atc atc aac gag tac ttc aac tcc atc aac gac tcc aag atc ttg tcc	147
Ile Ile Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser	
35 40 45	
ttg cag aac aag aag aac gcc ttg gtc gac acc tcc ggt tac aac gcc	195
Leu Gln Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala	
50 55 60	
gag gtc aga gtc ggt gac aac gtc cag ttg aac acc atc tac acc aac	243
Glu Val Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn	
65 70 75	
gac ttc aag ttg tcc tct tcc ggt gac aag atc atc gtc aac ttg aac	291
Asp Phe Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn	
80 85 90	
aac aac atc ttg tac tcc gcc atc tac gag aac tcc tct gtc tcc ttc	339
Asn Asn Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe	
95 100 105 110	
tgg atc aag atc tcc aag gac ttg acc aac tcc cac aac gag tac acc	387
Trp Ile Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr	
115 120 125	
atc atc aac tcc atc gag cag aac tcc ggt tgg aag ttg tgt atc cgt	435
Ile Ile Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg	
130 135 140	
aac ggt aac atc gag tgg atc ttg cag gac gtc aac cgt aag tac aag	483
Asn Gly Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys	
145 150 155	
tcc ttg atc ttc gac tac tcc gag tcc ttg tcc cac acc ggt tac acc	531
Ser Leu Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr	
160 165 170	
aac aag tgg ttc ttc gtc acc atc acc aac aac atc atg ggt tac atg	579
Asn Lys Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met	
175 180 185 190	
aag ttg tac atc aac ggt gag ttg aag cag tcc cag aag atc gag gac	627
Lys Leu Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp	
195 200 205	
ctg gac gag gtc aag ctg gac aag acc atc gtc ttc ggt atc gac gag	675
Leu Asp Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu	
210 215 220	
aac atc gac gag aac cag atg ttg tgg atc cgt gac ttc aac atc ttc	723
Asn Ile Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe	
225 230 235	

69

tcc aag gag ctg tcc aac gag gac atc aac atc gtc tac gag ggt cag 771
 Ser Lys Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln
 240 245 250

atc ctg agg aac gtc atc aag gac tac tgg ggt aac cca ctg aag ttc 819
 Ile Leu Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe
 255 260 265 270

gac acc gag tac tac atc atc aac gac aac tac atc gac cgt tac atc 867
 Asp Thr Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile
 275 280 285

gcc cca gag tcc aac gtc ctg gtc ctg gtc cag tac cct gac cgt tcc 915
 Ala Pro Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Arg Ser
 290 295 300

aag ctg tac acc ggt aac cct atc acc atc aag tcc gtc tcc gac aag 963
 Lys Leu Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys
 305 310 315

aac cct tac tcc cgt atc ctg aac ggt gac aac atc atc ctg cac atg 1011
 Asn Pro Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met
 320 325 330

ctg tac aac tcc cgt aag tac atg atc atc cgt gac acc gac acc atc 1059
 Leu Tyr Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile
 335 340 345 350

tac gcc acc cag ggt ggt gac tgt tcc cag aac tgt gtc tac gcc ctg 1107
 Tyr Ala Thr Gln Gly Gly Asp Cys Ser Gln Asn Cys Val Tyr Ala Leu
 355 360 365

aag ctg cag tcc aac ctg ggt aac tac ggt atc ggt atc ttc tcc atc 1155
 Lys Leu Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile
 370 375 380

aag aac atc gtc tcc aag aac aag tac tgc tcc cag atc ttc tcc tcc 1203
 Lys Asn Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser
 385 390 395

ttc cgt gag aac acc atg ctg ctg gcc gac atc tac aag cct tgg cgt 1251
 Phe Arg Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg
 400 405 410

ttc tcc ttc aag aac gcc tac act cct gtc gcc gtc acc aac tac gag 1299
 Phe Ser Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu
 415 420 425 430

acc aag ctg ctg tcc acc tcc tcc ttc tgg aag ttc atc tcc cgt gac 1347
 Thr Lys Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp
 435 440 445

cca ggt tgg gtc gag taataggaat tc 1374
 Pro Gly Trp Val Glu
 450

<210> 12
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTD Hc

<400> 12
Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Met Pro
1 5 10 15
Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile
20 25 30
Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln
35 40 45
Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val
50 55 60
Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe
65 70 75 80
Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn
85 90 95
Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile
100 105 110
Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile
115 120 125
Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly
130 135 140
Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys Ser Leu
145 150 155 160
Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys
165 170 175
Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu
180 185 190
Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp
195 200 205
Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile
210 215 220
Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys
225 230 235 240
Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln Ile Leu
245 250 255
Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe Asp Thr
260 265 270
Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile Ala Pro
275 280 285
Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Arg Ser Lys Leu
290 295 300
Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys Asn Pro
305 310 315 320
Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met Leu Tyr
325 330 335
Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile Tyr Ala
340 345 350
Thr Gln Gly Gly Asp Cys Ser Gln Asn Cys Val Tyr Ala Leu Lys Leu
355 360 365
Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile Lys Asn

370		375		380
Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser Phe Arg				
385		390		400
Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg Phe Ser				
	405		410	415
Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu Thr Lys				
	420		425	430
Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp Pro Gly				
	435		440	445
Trp Val Glu				
450				

<210> 13
 <211> 1400
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (10)...(1356)

<400> 13
 gaattcacc atg gga gag agt cag caa gaa cta aat tct atg gta act gat 51
 Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp

1	5	10	
acc cta aat aat agt att cct ttt aag ctt tct tct tat aca gat gat			99
Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp			
15	20	25	30
aaa att tta att tcc tac ttc aac aag ttc ttc aag aga att aag tct			147
Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser			
	35	40	45
tct tcc gtt tta aac atg aga tac aag aat gat aaa tac gtc gac act			195
Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr			
	50	55	60
tcc ggt tac gac tcc aat atc aac att aac ggt gac gtg tac aag tac			243
Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr			
	65	70	75
cca act aac aaa aac caa ttc ggt atc tac aac gac aag ctt act gag			291
Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu			
	80	85	90
ctg aac atc tct caa aac gac tac att atc tac gac aac aag tac aag			339
Leu Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys			
	95	100	105
aac ttc tct att tct ttc tgg gtc agg att cct aac tac gac aac aag			387
Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys			
	115	120	125

atc gtc aac gtt aac aac gag tac act atc atc aac tgt atg aga gac 435
 Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp
 130 135 140

aac aac tcc ggt tgg aag gtc tct ctt aac cac aac gag atc att tgg 483
 Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp
 145 150 155

acc ttg caa gac aac gca ggt att aac caa aag tta gca ttc aac tac 531
 Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr
 160 165 170

ggt aac gca aac ggt att tct gac tac atc aac aag tgg att ttc gtc 579
 Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val
 175 180 185 190

act atc act aac gac aga tta ggt gac tct aag ctt tac att aac ggt 627
 Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly
 195 200 205

aac tta atc gac caa aag tcc att tta aac tta ggt aac att cac gtt 675
 Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val
 210 215 220

tct gac aac atc tta ttc aag atc gtt aac tgc agt tac acc aga tac 723
 Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr
 225 230 235

att ggc att aga tac ttc aac att ttc gac aag gag tta gac gag acc 771
 Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr
 240 245 250

gag att caa act tta tac agc aac gaa cct aac acc aat att ttg aag 819
 Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys
 255 260 265 270

gac ttc tgg ggt aac tac ttg ctt tac gac aag gaa tac tac tta tta 867
 Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu
 275 280 285

aac gtg tta aag cca aac aac ttc att gat agg aga aag gat tct act 915
 Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr
 290 295 300

tta agc att aac aac atc aga agc act att ctt tta gct aac aga tta 963
 Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu
 305 310 315

tac tct ggt atc aag gtt aag atc caa aga gtt aac aac tct tct act 1011
 Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr
 320 325 330

aac gat aac ctt gtt aga aag aac gat cag gtc tat att aac ttc gtc 1059
 Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val
 335 340 345 350

gct agc aag act cac tta ttc cca tta tat gct gat acc gct acc acc 1107

Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr	
355 360 365	
aac aag gag aag acc atc aag atc tcc tcc tct ggc aac aga ttt aac	1155
Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn	
370 375 380	
caa gtc gtc gtt atg aac tcc gtc ggt aac aac tgt acc atg aac ttt	1203
Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe	
385 390 395	
aaa aat aat aat gga aat aat att ggg ttg tta ggt ttc aag gca gat	1251
Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp	
400 405 410	
act gta gtt gct agt act tgg tat tat acc cac atg aga gat cac acc	1299
Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr	
415 420 425 430	
aac agc aat gga tgt ttt tgg aac ttt att tct gaa gaa cat gga tgg	1347
Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp	
435 440 445	
caa gaa aaa taatagggat ccgcggccgc acgcgtcccg ggactagtga	1396
Gln Glu Lys	

attc 1400

<210> 14

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BONTÉ Hc

<400> 14

Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp Thr Leu	
1 5 10 15	
Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp Lys Ile	
20 25 30	
Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser Ser Ser	
35 40 45	
Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr Ser Gly	
50 55 60	
Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr Pro Thr	
65 70 75 80	
Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu Leu Asn	
85 90 95	
Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys Asn Phe	
100 105 110	
Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys Ile Val	
115 120 125	
Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp Asn Asn	
130 135 140	

Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp Thr Leu
 145 150 155 160
 Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr Gly Asn
 165 170 175
 Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile
 180 185 190
 Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly Asn Leu
 195 200 205
 Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val Ser Asp
 210 215 220
 Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr Ile Gly
 225 230 235 240
 Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr Glu Ile
 245 250 255
 Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys Asp Phe
 260 265 270
 Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu Asn Val
 275 280 285
 Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr Leu Ser
 290 295 300
 Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser
 305 310 315 320
 Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr Asn Asp
 325 330 335
 Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val Ala Ser
 340 345 350
 Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr Asn Lys
 355 360 365
 Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn Gln Val
 370 375 380
 Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe Lys Asn
 385 390 395 400
 Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp Thr Val
 405 410 415
 Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr Asn Ser
 420 425 430
 Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp Gln Glu
 435 440 445
 Lys

<210> 15
 <211> 1317
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (10)...(1305)

<400> 15
 gaattcacg atg tcc tac acc aac gac aag atc ctg atc ttg tac ttc aac 51
 Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
 1 5 10

aag ctg tac aag aag atc aag gac aac tcc atc ttg gac atg aga tac	99
Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr	
15 20 25 30	
gaa aac aat aag ttc atc gac atc tcc ggt tac ggt tcc aac atc tcc	147
Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser	
35 40 45	
atc aac ggt gac gtc tac atc tac tcc acc aat aga aac cag ttc gga	195
Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly	
50 55 60	
atc tac tcc tcc aag cct tcc gag gtc aac atc gct cag aac aac gac	243
Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp	
65 70 75	
atc atc tac aac gga aga tac cag aac ttc tcc atc tcc ttc tgg gtc	291
Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val	
80 85 90	
cgt atc cca aag tac ttc aac aag gtc aac ctg aat aac gag tac acc	339
Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr	
95 100 105 110	
atc atc gac tgc atc cgt aac aat aac tcc gga tgg aag atc tcc ctg	387
Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu	
115 120 125	
aac tac aac aag atc atc tgg acc ctg cag gac acc gcc ggt aac aat	435
Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn	
130 135 140	
cag aag ttg gtc ttc aac tac acc cag atg atc tcc atc tcc gac tac	483
Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr	
145 150 155	
atc aac aag tgg atc ttc gtc acc atc acc aat aac cgt ttg gga aac	531
Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn	
160 165 170	
tcc aga atc tac atc aac ggt aac ttg atc gac gag aag tcc atc tcc	579
Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser	
175 180 185 190	
aac ttg ggt gac atc cac gtc tcc gac aac att ttg ttc aag atc gtc	627
Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val	
195 200 205	
ggt tgt aac gac acc cgt tac gtc ggg atc cgt tac ttc aaa gtc ttc	675
Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe	
210 215 220	
gac act gag ttg ggt aag acc gag atc gag acc ttg tac tcc gac gag	723
Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu	
225 230 235	

Ca

cct gac cca tcc atc ctg aag gac ttc tgg ggt aac tac ctg ctg tac 771
Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr
240 245 250

aac aaa cgt tac tac ttg ctg aac ttg ttg cgt acc gac aag tcc atc 819
Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile
255 260 265 270

acc cag aac tcc aac ttc ttg aac atc aac cag cag aga ggt gtc tac 867
Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr
275 280 285

cag aag cca aac atc ttc tcc aac acc aga ttg tac acc gga gtc gag 915
Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu
290 295 300

gtc att atc aga aag aac gga tct act gat att tcc aac acc gat aac 963
Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn
305 310 315

ttc gtc aga aag aac gat ctg gct tac atc aac gtt gtc gac aga gat 1011
Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp
320 325 330

gtc gaa tac cgt ctg tac gcc gat atc tct atc gcc aaa cct gaa aag 1059
Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys
335 340 345 350

atc atc aag ctg atc cgt acc tct aac tct aac aac tct ctg gga caa 1107
Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln
355 360 365

atc atc gtc atg gac tcc atc ggt aat aac tgt acc atg aac ttc cag 1155
Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln
370 375 380

aac aac aac ggt gga aac atc ggt ttg ttg ggt ttc cac tcc aac aac 1203
Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn
385 390 395

ttg gtc gct tcc tcc tgg tac tac aac aac atc cgt aag aac acc tcc 1251
Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser
400 405 410

tcc aac ggt tgc ttc tgg tcc ttc atc tcc aag gag cac ggt tgg cag 1299
Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln
415 420 425 430

gag aac taataggaat tc 1317
Glu Asn

<210> 16
<211> 432
<212> PRT
<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTF Hc

<400> 16

Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu
1 5 10 15
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn
20 25 30
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn
35 40 45
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr
50 55 60
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile
65 70 75 80
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile
85 90 95
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
100 105 110
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
115 120 125
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
130 135 140
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
145 150 155 160
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
165 170 175
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
180 185 190
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
195 200 205
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
210 215 220
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
225 230 235 240
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
245 250 255
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
260 265 270
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
275 280 285
Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
290 295 300
Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
305 310 315 320
Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
325 330 335
Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
340 345 350
Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
355 360 365
Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
370 375 380
Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
385 390 395 400
Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn

				405						410					415				
Gly	Cys	Phe	Trp	Ser	Phe	Ile	Ser	Lys	Glu	His	Gly	Trp	Gln	Glu	Asn				
			420					425					430						

<210> 17
 <211> 1368
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (10)...(1356)

<400> 17
 gaattcacg atg aag gac acc atc ctg atc cag gtc ttc aac aac tac atc 51
 Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile
 1 5 10

tcc aac atc tcc tcc aac gcc atc ctg tcc ctg tcc tac cgt ggt ggt 99
 Ser Asn Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly
 15 20 25 30

cgt ctg atc gac tcc tcc ggt tac gga gcc acc atg aac gtc ggt tcc 147
 Arg Leu Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser
 35 40 45

gac gtc atc ttc aac gac atc ggt aac ggt cag ttc aag ctg aac aac 195
 Asp Val Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn
 50 55 60

tcc gag aac tcc aac atc acc gcc cac cag tcc aag ttc gtc gtc tac 243
 Ser Glu Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr
 65 70 75

gac tcc atg ttc gac aac ttc tcc atc aac ttc tgg gtc cgt acc cca 291
 Asp Ser Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro
 80 85 90

aag tac aac aac aac gac atc cag acc tac ctg cag aac gag tac acc 339
 Lys Tyr Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr
 95 100 105 110

atc atc tcc tgt atc aag aac gac tcc ggt tgg aag gtc tcc atc aag 387
 Ile Ile Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys
 115 120 125

gga aac cgt atc atc tgg acc ctg atc gac gtc aac gcc aag tcc aag 435
 Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys
 130 135 140

tcc atc ttc ttc gag tac tcc atc aag gac aac atc tcc gac tac atc 483
 Ser Ile Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile
 145 150 155

aac aag tgg ttc tcc atc acc atc acc aac gac cgt ctg ggt aac gcc 531
 Asn Lys Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala
 160 165 170

aac atc tac atc aac ggt tcc ctg aag aag tcc gag aag atc ctg aac 579
 Asn Ile Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn
 175 180 185 190

ctg gac cgt atc aac tcc tcc aac gac atc gac ttc aag ctg atc aac 627
 Leu Asp Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn
 195 200 205

tgt acc gac acc acc aag ttc gtc tgg atc aag gac ttc aac atc ttc 675
 Cys Thr Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe
 210 215 220

ggt cgt gag ctg aac gcc acc gag gtc tcc tcc ctg tac tgg atc cag 723
 Gly Arg Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln
 225 230 235

tcc tcc acc aac acc ctg aag gac ttc tgg gga aac cca ctg cgt tac 771
 Ser Ser Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr
 240 245 250

gac acc cag tac tac ctg ttc aac cag ggt atg cag aac atc tac atc 819
 Asp Thr Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile
 255 260 265 270

aag tac ttc tcc aag gcc tcc atg ggt gag acc gcc cct cgt acc aac 867
 Lys Tyr Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn
 275 280 285

ttc aac aac gcc gcc atc aac tac cag aac ctg tac ctg ggt ctg cgt 915
 Phe Asn Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg
 290 295 300

ttc atc atc aag aag gcc tcc aac tcc cgt aac atc aac aac gac aac 963
 Phe Ile Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn
 305 310 315

atc gtc cgt gag ggt gac tac atc tac ctg aac atc gac aac atc tcc 1011
 Ile Val Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser
 320 325 330

gac gag tcc tac cgt gtc tac gtc ctg gtc aac tcc aag gag atc cag 1059
 Asp Glu Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln
 335 340 345 350

acc cag ctg ttc ctg gcc cca atc aac gac gac cct acc ttc tac gac 1107
 Thr Gln Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp
 355 360 365

gtc ctg cag atc aag aag tac tac gag aag acc acc tac aac tgt cag 1155
 Val Leu Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln
 370 375 380

atc ctg tgc gag aag gac acc aag acc ttc gga ctg ttc ggt atc ggt 1203

Ile	Leu	Cys	Glu	Lys	Asp	Thr	Lys	Thr	Phe	Gly	Leu	Phe	Gly	Ile	Gly		
		385						390					395				
aag	ttc	gtc	aag	gac	tac	ggg	tac	gtc	tgg	gac	acc	tac	gac	aac	tac	1251	
Lys	Phe	Val	Lys	Asp	Tyr	Gly	Tyr	Val	Trp	Asp	Thr	Tyr	Asp	Asn	Tyr		
	400					405					410						
ttc	tgt	atc	tcc	cag	tgg	tac	ctg	cgt	cgt	atc	tcc	gag	aac	atc	aac	1299	
Phe	Cys	Ile	Ser	Gln	Trp	Tyr	Leu	Arg	Arg	Ile	Ser	Glu	Asn	Ile	Asn		
415					420				425					430			
aag	ctg	cgt	ctg	gga	tgt	aac	tgg	cag	ttc	atc	cca	gtc	gac	gag	ggg	1347	
Lys	Leu	Arg	Leu	Gly	Cys	Asn	Trp	Gln	Phe	Ile	Pro	Val	Asp	Glu	Gly		
				435					440					445			
tgg	acc	gag	taataggaat	tc												1368	
Trp	Thr	Glu															

<210> 18
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based
 on BoNTG Hc

CG

<400> 18																	
Met	Lys	Asp	Thr	Ile	Leu	Ile	Gln	Val	Phe	Asn	Asn	Tyr	Ile	Ser	Asn		
1				5					10					15			
Ile	Ser	Ser	Asn	Ala	Ile	Leu	Ser	Leu	Ser	Tyr	Arg	Gly	Gly	Arg	Leu		
			20					25					30				
Ile	Asp	Ser	Ser	Gly	Tyr	Gly	Ala	Thr	Met	Asn	Val	Gly	Ser	Asp	Val		
		35				40						45					
Ile	Phe	Asn	Asp	Ile	Gly	Asn	Gly	Gln	Phe	Lys	Leu	Asn	Asn	Ser	Glu		
	50					55					60						
Asn	Ser	Asn	Ile	Thr	Ala	His	Gln	Ser	Lys	Phe	Val	Val	Tyr	Asp	Ser		
65				70					75					80			
Met	Phe	Asp	Asn	Phe	Ser	Ile	Asn	Phe	Trp	Val	Arg	Thr	Pro	Lys	Tyr		
			85					90					95				
Asn	Asn	Asn	Asp	Ile	Gln	Thr	Tyr	Leu	Gln	Asn	Glu	Tyr	Thr	Ile	Ile		
			100					105					110				
Ser	Cys	Ile	Lys	Asn	Asp	Ser	Gly	Trp	Lys	Val	Ser	Ile	Lys	Gly	Asn		
	115						120					125					
Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Val	Asn	Ala	Lys	Ser	Lys	Ser	Ile		
	130					135					140						
Phe	Phe	Glu	Tyr	Ser	Ile	Lys	Asp	Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Lys		
145					150				155					160			
Trp	Phe	Ser	Ile	Thr	Ile	Thr	Asn	Asp	Arg	Leu	Gly	Asn	Ala	Asn	Ile		
			165					170					175				
Tyr	Ile	Asn	Gly	Ser	Leu	Lys	Lys	Ser	Glu	Lys	Ile	Leu	Asn	Leu	Asp		
		180						185				190					
Arg	Ile	Asn	Ser	Ser	Asn	Asp	Ile	Asp	Phe	Lys	Leu	Ile	Asn	Cys	Thr		
	195					200					205						
Asp	Thr	Thr	Lys	Phe	Val	Trp	Ile	Lys	Asp	Phe	Asn	Ile	Phe	Gly	Arg		

210 215 220
 Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln Ser Ser
 225 230 235 240
 Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr
 245 250 255
 Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile Lys Tyr
 260 265 270
 Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn Phe Asn
 275 280 285
 Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg Phe Ile
 290 295 300
 Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn Ile Val
 305 310 315 320
 Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu
 325 330 335
 Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln Thr Gln
 340 345 350
 Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp Val Leu
 355 360 365
 Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln Ile Leu
 370 375 380
 Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly Lys Phe
 385 390 395 400
 Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr Phe Cys
 405 410 415
 Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn Lys Leu
 420 425 430
 Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly Trp Thr
 435 440 445
 Glu

<210> 19
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (1)...(1239)

<400> 19
 atg gct ctg aac gac ctg tgc atc aaa gtt aac aac tgg gac ctg ttc 48
 Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
 1 5 10 15

 ttc tcc ccg tct gaa gac aac ttc act aac gac ctg aac aaa ggc gaa 96
 Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
 20 25 30

 gaa atc acc tcc gac act aac atc gaa gct gct gaa gaa aac atc tct 144
 Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
 35 40 45

ctg gac ctg atc cag cag tac tac ctg act ttc aac ttc gac aac gaa	192
Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu	
50 55 60	
ccg gaa aac atc tcc atc gaa aac ctg tct tcc gac atc atc ggt cag	240
Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln	
65 70 75 80	
ctg gaa ctg atg ccg aac atc gaa cgc ttc ccg aac ggc aag aaa tac	288
Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr	
85 90 95	
gaa ctg gac aaa tac acc atg ttc cac tac ctg cgt gct cag gaa ttc	336
Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe	
100 105 110	
gaa cac ggt aaa tct cgt atc gct ctg act aac tcc gtt aac gaa gct	384
Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala	
115 120 125	
ctg ctg aac ccg tct cgc gtt tac acc ttc ttc tct tcc gac tac gtt	432
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val	
130 135 140	
aag aaa gtt aac aaa gct act gaa gct gct atg ttc ctg ggt tgg gtt	480
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val	
145 150 155 160	
gaa cag ctg gtt tac gac ttc acc gac gaa act tct gaa gtt tcc acc	528
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr	
165 170 175	
act gac aaa atc gct gac atc act atc atc atc ccg tac atc ggc ccg	576
Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro	
180 185 190	
gct ctg aac atc ggt aac atg ctg tac aaa gac gac ttc gtt ggt gct	624
Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala	
195 200 205	
ctg atc ttc tct ggc gct gtt atc ctg ctg gaa ttc atc ccg gaa atc	672
Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile	
210 215 220	
gct atc ccg gtt ctg ggt acc ttc gct ctg gtt tcc tac atc gct aac	720
Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn	
225 230 235 240	
aaa gtt ctg act gtt cag acc atc gac aac gct ctg tct aaa cgt aac	768
Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn	
245 250 255	
gaa aaa tgg gac gaa gtt tac aaa tac atc gtt act aac tgg ctg gct	816
Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala	
260 265 270	
aaa gtt aac act cag atc gac ctg atc cgt aag aag atg aaa gaa gct	864

CG

Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala
 275 280 285

ctg gaa aac cag gct gaa gct act aaa gct atc atc aac tac cag tac 912
 Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr
 290 295 300

aac cag tac acc gaa gaa gaa aag aac aac atc aac ttc aac atc gat 960
 Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp
 305 310 315 320

gac ctg tcc tct aaa ctg aac gaa tcc atc aac aaa gct atg atc aac 1008
 Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn
 325 330 335

atc aac aaa ttc ctg aac cag tgc tct gtt tcc tac ctg atg aac tct 1056
 Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser
 340 345 350

atg atc ccg tac ggc gtt aaa cgc ctg gaa gac ttc gac gct tcc ctg 1104
 Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu
 355 360 365

aaa gac gct ctg ctg aaa tac atc cgt gac aac tac ggt act ctg atc 1152
 Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile
 370 375 380

ggc cag gtt gac cgt ctg aaa gac aag gtt aac aac acc ctg tct act 1200
 Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr
 385 390 395 400

gac atc ccg ttc cag ctg tcc aaa tac gtt gac aac cag taa 1242
 Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln
 405 410

<210> 20

<211> 413

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
 on BoNTA Hn

<400> 20

Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
 1 5 10 15
 Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
 20 25 30
 Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
 35 40 45
 Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu
 50 55 60
 Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln
 65 70 75 80
 Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr

				85					90					95			
Glu	Leu	Asp	Lys	Tyr	Thr	Met	Phe	His	Tyr	Leu	Arg	Ala	Gln	Glu	Phe		
			100					105					110				
Glu	His	Gly	Lys	Ser	Arg	Ile	Ala	Leu	Thr	Asn	Ser	Val	Asn	Glu	Ala		
		115					120					125					
Leu	Leu	Asn	Pro	Ser	Arg	Val	Tyr	Thr	Phe	Phe	Ser	Ser	Asp	Tyr	Val		
	130					135					140						
Lys	Lys	Val	Asn	Lys	Ala	Thr	Glu	Ala	Ala	Met	Phe	Leu	Gly	Trp	Val		
145				150					155						160		
Glu	Gln	Leu	Val	Tyr	Asp	Phe	Thr	Asp	Glu	Thr	Ser	Glu	Val	Ser	Thr		
			165					170						175			
Thr	Asp	Lys	Ile	Ala	Asp	Ile	Thr	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro		
		180					185						190				
Ala	Leu	Asn	Ile	Gly	Asn	Met	Leu	Tyr	Lys	Asp	Asp	Phe	Val	Gly	Ala		
		195					200					205					
Leu	Ile	Phe	Ser	Gly	Ala	Val	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Ile		
	210					215				220							
Ala	Ile	Pro	Val	Leu	Gly	Thr	Phe	Ala	Leu	Val	Ser	Tyr	Ile	Ala	Asn		
225				230					235						240		
Lys	Val	Leu	Thr	Val	Gln	Thr	Ile	Asp	Asn	Ala	Leu	Ser	Lys	Arg	Asn		
			245					250						255			
Glu	Lys	Trp	Asp	Glu	Val	Tyr	Lys	Tyr	Ile	Val	Thr	Asn	Trp	Leu	Ala		
		260				265						270					
Lys	Val	Asn	Thr	Gln	Ile	Asp	Leu	Ile	Arg	Lys	Lys	Met	Lys	Glu	Ala		
		275				280						285					
Leu	Glu	Asn	Gln	Ala	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asn	Tyr	Gln	Tyr		
	290					295					300						
Asn	Gln	Tyr	Thr	Glu	Glu	Glu	Lys	Asn	Asn	Ile	Asn	Phe	Asn	Ile	Asp		
305				310						315					320		
Asp	Leu	Ser	Ser	Lys	Leu	Asn	Glu	Ser	Ile	Asn	Lys	Ala	Met	Ile	Asn		
			325					330						335			
Ile	Asn	Lys	Phe	Leu	Asn	Gln	Cys	Ser	Val	Ser	Tyr	Leu	Met	Asn	Ser		
		340					345						350				
Met	Ile	Pro	Tyr	Gly	Val	Lys	Arg	Leu	Glu	Asp	Phe	Asp	Ala	Ser	Leu		
		355					360					365					
Lys	Asp	Ala	Leu	Leu	Lys	Tyr	Ile	Arg	Asp	Asn	Tyr	Gly	Thr	Leu	Ile		
	370					375					380						
Gly	Gln	Val	Asp	Arg	Leu	Lys	Asp	Lys	Val	Asn	Asn	Thr	Leu	Ser	Thr		
385				390					395						400		
Asp	Ile	Pro	Phe	Gln	Leu	Ser	Lys	Tyr	Val	Asp	Asn	Gln					
			405					410									

<210> 21
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (1)...(1239)

<400> 21
 atg gct cca gga atc tgt atc gac gtc gac aac gag gac ttg ttc ttc 48
 Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe

1	5	10	15	
atc gct gac aag aac tcc ttc tcc gac gac ttg tcc aag aac gag aga	96			
Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg				
20 25 30				
atc gag tac aac acc cag tcc aac tac atc gag aac gac ttc cca atc	144			
Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile				
35 40 45				
aac gag ttg atc ttg gac acc gac ttg atc tcc aag atc gag ttg cca	192			
Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro				
50 55 60				
tcc gag aac acc gag tcc ttg act gac ttc aac gtc gac gtc cca gtc	240			
Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val				
65 70 75 80				
tac gag aag caa cca gct atc aag aag att ttc acc gac gag aac acc	288			
Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr				
85 90 95				
atc ttc caa tac ctg tac tct cag acc ttc cct ttg gac atc aga gac	336			
Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp				
100 105 110				
atc tcc ttg acc tct tcc ttc gac gac gcc ctg ctg ttc tcc aac aag	384			
Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys				
115 120 125				
gtc tac tcc ttc ttc tcc atg gac tac atc aag act gct aac aag gtc	432			
Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val				
130 135 140				
gtc gag gcc ggt ttg ttc gct ggt tgg gtc aag cag atc gtc aac gat	480			
Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp				
145 150 155 160				
ttc gtc atc gag gct aac aag tcc aac acc atg gac aag att gcc gac	528			
Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp				
165 170 175				
atc tcc ttg att gtc cca tac atc ggt ttg gcc ttg aac gtc ggt aac	576			
Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn				
180 185 190				
gag acc gcc aag ggt aac ttc gag aac gct ttc gag atc gct ggt gcc	624			
Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala				
195 200 205				
tcc atc ttg ttg gag ttc atc cca gag ttg ttg atc cca gtc gtc ggt	672			
Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly				
210 215 220				
gcc ttc ttg ttg gag tcc tac atc gac aac aag aac aag atc atc aag	720			
Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys				
225 230 235 240				

Ca

acc atc gac aac gct ttg acc aag aga aac gag aag tgg tcc gac atg	768
Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met	
245 250 255	
tac ggt ttg atc gtc gcc caa tgg ttg tcc acc gtc aac acc caa ttc	816
Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe	
260 265 270	
tac acc atc aag gag ggt atg tac aag gcc ttg aac tac cag gcc caa	864
Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln	
275 280 285	
gct ttg gag gag atc atc aag tac aga tac aac atc tac tcc gag aag	912
Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys	
290 295 300	
gag aag tcc aac att aac atc gac ttc aac gac atc aac tcc aag ctg	960
Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu	
305 310 315 320	
aac gag ggt att aac cag gcc atc gac aac atc aac aac ttc atc aac	1008
Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn	
325 330 335	
ggt tgt tcc gtc tcc tac ttg atg aag aag atg att cca ttg gcc gtc	1056
Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val	
340 345 350	
gag aag ttg ttg gac ttc gac aac acc ctg aag aag aac ttg ttg aac	1104
Glu Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn	
355 360 365	
tac atc gac gag aac aag ttg tac ttg atc ggt tcc gct gag tac gag	1152
Tyr Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu	
370 375 380	
aag tcc aag gtc aac aag tac ttg aag acc atc atg cca ttc gac ttg	1200
Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu	
385 390 395 400	
tcc atc tac acc aac gac acc atc ttg atc gag atg ttc taa	1242
Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe	
405 410	

<210> 22

<211> 413

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTB Hn

<400> 22

Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe

1				5					10					15			
Ile	Ala	Asp	Lys	Asn	Ser	Phe	Ser	Asp	Asp	Leu	Ser	Lys	Asn	Glu	Arg		
			20					25					30				
Ile	Glu	Tyr	Asn	Thr	Gln	Ser	Asn	Tyr	Ile	Glu	Asn	Asp	Phe	Pro	Ile		
		35					40					45					
Asn	Glu	Leu	Ile	Leu	Asp	Thr	Asp	Leu	Ile	Ser	Lys	Ile	Glu	Leu	Pro		
	50					55					60						
Ser	Glu	Asn	Thr	Glu	Ser	Leu	Thr	Asp	Phe	Asn	Val	Asp	Val	Pro	Val		
65					70					75					80		
Tyr	Glu	Lys	Gln	Pro	Ala	Ile	Lys	Lys	Ile	Phe	Thr	Asp	Glu	Asn	Thr		
			85						90					95			
Ile	Phe	Gln	Tyr	Leu	Tyr	Ser	Gln	Thr	Phe	Pro	Leu	Asp	Ile	Arg	Asp		
		100						105					110				
Ile	Ser	Leu	Thr	Ser	Ser	Phe	Asp	Asp	Ala	Leu	Leu	Phe	Ser	Asn	Lys		
		115					120					125					
Val	Tyr	Ser	Phe	Phe	Ser	Met	Asp	Tyr	Ile	Lys	Thr	Ala	Asn	Lys	Val		
	130					135					140						
Val	Glu	Ala	Gly	Leu	Phe	Ala	Gly	Trp	Val	Lys	Gln	Ile	Val	Asn	Asp		
145					150					155					160		
Phe	Val	Ile	Glu	Ala	Asn	Lys	Ser	Asn	Thr	Met	Asp	Lys	Ile	Ala	Asp		
			165					170						175			
Ile	Ser	Leu	Ile	Val	Pro	Tyr	Ile	Gly	Leu	Ala	Leu	Asn	Val	Gly	Asn		
		180						185					190				
Glu	Thr	Ala	Lys	Gly	Asn	Phe	Glu	Asn	Ala	Phe	Glu	Ile	Ala	Gly	Ala		
		195					200					205					
Ser	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Leu	Leu	Ile	Pro	Val	Val	Gly		
	210					215					220						
Ala	Phe	Leu	Leu	Glu	Ser	Tyr	Ile	Asp	Asn	Lys	Asn	Lys	Ile	Ile	Lys		
225					230					235					240		
Thr	Ile	Asp	Asn	Ala	Leu	Thr	Lys	Arg	Asn	Glu	Lys	Trp	Ser	Asp	Met		
			245						250					255			
Tyr	Gly	Leu	Ile	Val	Ala	Gln	Trp	Leu	Ser	Thr	Val	Asn	Thr	Gln	Phe		
		260						265					270				
Tyr	Thr	Ile	Lys	Glu	Gly	Met	Tyr	Lys	Ala	Leu	Asn	Tyr	Gln	Ala	Gln		
		275					280					285					
Ala	Leu	Glu	Glu	Ile	Ile	Lys	Tyr	Arg	Tyr	Asn	Ile	Tyr	Ser	Glu	Lys		
	290					295					300						
Glu	Lys	Ser	Asn	Ile	Asn	Ile	Asp	Phe	Asn	Asp	Ile	Asn	Ser	Lys	Leu		
305					310					315					320		
Asn	Glu	Gly	Ile	Asn	Gln	Ala	Ile	Asp	Asn	Ile	Asn	Asn	Phe	Ile	Asn		
			325					330						335			
Gly	Cys	Ser	Val	Ser	Tyr	Leu	Met	Lys	Lys	Met	Ile	Pro	Leu	Ala	Val		
		340						345					350				
Glu	Lys	Leu	Leu	Asp	Phe	Asp	Asn	Thr	Leu	Lys	Lys	Asn	Leu	Leu	Asn		
	355						360					365					
Tyr	Ile	Asp	Glu	Asn	Lys	Leu	Tyr	Leu	Ile	Gly	Ser	Ala	Glu	Tyr	Glu		
	370					375					380						
Lys	Ser	Lys	Val	Asn	Lys	Tyr	Leu	Lys	Thr	Ile	Met	Pro	Phe	Asp	Leu		
385					390					395					400		
Ser	Ile	Tyr	Thr	Asn	Asp	Thr	Ile	Leu	Ile	Glu	Met	Phe					
			405						410								

<210> 23
 <211> 1200
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hc

<221> CDS

<222> (1)...(1197)

<400> 23

atg tcc ctg tac aac aag acc ctt gac tgt aga gag ctg ctg gtg aag 48
Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
1 5 10 15

aac act gac ctg cca ttc atc ggt gac atc agt gac gtg aag act gac 96
Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp
20 25 30

atc ttc ctg cgt aag gac atc aac gag gag act gag gtg atc tac tac 144
Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr
35 40 45

cca gac aac gtg tca gta gac caa gtg atc ctc agt aag aac acc tcc 192
Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser
50 55 60

gag cat gga caa cta gac ctg ctc tac cct agt atc gac agt gag agt 240
Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser
65 70 75 80

gag atc ctg cca ggg gag aat caa gtc ttc tac gac aac cgt acc cag 288
Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln
85 90 95

aac gtg gac tac ctg aac tcc tac tac tac cta gag tct cag aag ctg 336
Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu
100 105 110

agt gac aac gtg gag gac ttc act ttc acg cgt tca atc gag gag gct 384
Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala
115 120 125

ctg gac aac agt gca aag gtg tac act tac ttc cct acc ctg gct aac 432
Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn
130 135 140

aag gtg aat gcc ggt gtg caa ggt ggt ctg ttc ctg atg tgg gca aac 480
Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn
145 150 155 160

gac gtg gtt gag gac ttc act acc aac atc ctg cgt aag gac aca ctg 528
Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu
165 170 175

gac aag atc tca gat gtg tca gct atc atc ccc tac atc gga ccc gca 576
Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala
180 185 190

ctg aac atc tcc aac tct gtg cgt cgt gga aac ttc act gag gca ttc 624

Leu	Asn	Ile	Ser	Asn	Ser	Val	Arg	Arg	Gly	Asn	Phe	Thr	Glu	Ala	Phe	
	195						200					205				
gca	gtc	act	ggg	gtc	acc	atc	ctg	ctg	gag	gca	ttc	cct	gag	ttc	aca	672
Ala	Val	Thr	Gly	Val	Thr	Ile	Leu	Leu	Glu	Ala	Phe	Pro	Glu	Phe	Thr	
	210					215				220						
atc	cct	gct	ctg	ggg	gca	ttc	gtg	atc	tac	agt	aag	gtc	cag	gag	cga	720
Ile	Pro	Ala	Leu	Gly	Ala	Phe	Val	Ile	Tyr	Ser	Lys	Val	Gln	Glu	Arg	
225				230				235						240		
aac	gag	atc	atc	aag	acc	atc	gac	aac	tgt	ctg	gag	cag	agg	atc	aag	768
Asn	Glu	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Cys	Leu	Glu	Gln	Arg	Ile	Lys	
				245				250						255		
aga	tgg	aag	gac	tcc	tac	gag	tgg	atg	atg	gga	acg	tgg	ttg	tcc	agg	816
Arg	Trp	Lys	Asp	Ser	Tyr	Glu	Trp	Met	Met	Gly	Thr	Trp	Leu	Ser	Arg	
			260					265					270			
atc	atc	acc	cag	ttc	aac	aac	atc	tcc	tac	cag	atg	tac	gac	tcc	ctg	864
Ile	Ile	Thr	Gln	Phe	Asn	Asn	Ile	Ser	Tyr	Gln	Met	Tyr	Asp	Ser	Leu	
		275					280					285				
aac	tac	cag	gca	ggg	gca	atc	aag	gct	aag	atc	gac	ctg	gag	tac	aag	912
Asn	Tyr	Gln	Ala	Gly	Ala	Ile	Lys	Ala	Lys	Ile	Asp	Leu	Glu	Tyr	Lys	
	290					295					300					
aag	tac	tcc	gga	agc	gac	aag	gag	aac	atc	aag	agc	cag	gtt	gag	aac	960
Lys	Tyr	Ser	Gly	Ser	Asp	Lys	Glu	Asn	Ile	Lys	Ser	Gln	Val	Glu	Asn	
305					310				315					320		
ctg	aag	aac	agt	ctg	gac	gtc	aag	atc	tcg	gag	gca	atg	aac	aac	atc	1008
Leu	Lys	Asn	Ser	Leu	Asp	Val	Lys	Ile	Ser	Glu	Ala	Met	Asn	Asn	Ile	
				325					330					335		
aac	aag	ttc	atc	cga	gag	tgc	tcc	gtc	acc	tac	ctg	ttc	aag	aac	atg	1056
Asn	Lys	Phe	Ile	Arg	Glu	Cys	Ser	Val	Thr	Tyr	Leu	Phe	Lys	Asn	Met	
			340					345					350			
ctg	cct	aag	gtc	atc	gac	gag	ctg	aac	gag	ttc	gac	cga	aac	acc	aag	1104
Leu	Pro	Lys	Val	Ile	Asp	Glu	Leu	Asn	Glu	Phe	Asp	Arg	Asn	Thr	Lys	
		355					360					365				
gca	aag	ctg	atc	aac	ctg	atc	gac	tcc	cat	aac	atc	atc	ctg	gtc	ggg	1152
Ala	Lys	Leu	Ile	Asn	Leu	Ile	Asp	Ser	His	Asn	Ile	Ile	Leu	Val	Gly	
	370					375					380					
gag	gtc	gac	aag	ctg	aag	gca	aag	gta	aac	aac	agc	ttc	cag	aac		1197
Glu	Val	Asp	Lys	Leu	Lys	Ala	Lys	Val	Asn	Asn	Ser	Phe	Gln	Asn		
385					390					395						
taa																1200

<210> 24

<211> 399

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTC Hn

<400> 24

Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
1 5 10 15
Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp
20 25 30
Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr
35 40 45
Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser
50 55 60
Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser
65 70 75 80
Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln
85 90 95
Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu
100 105 110
Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala
115 120 125
Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn
130 135 140
Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn
145 150 155 160
Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu
165 170 175
Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala
180 185 190
Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe
195 200 205
Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr
210 215 220
Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg
225 230 235 240
Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys
245 250 255
Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg
260 265 270
Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu
275 280 285
Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys
290 295 300
Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn
305 310 315 320
Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile
325 330 335
Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met
340 345 350
Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys
355 360 365
Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly
370 375 380
Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn
385 390 395

<210> 25
 <211> 1161
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (1)...(1158)

<400> 25
 atg gcc aac tcc cgt gac gac tcc acc tgc atc aag gtc aag aac aac 48
 Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
 1 5 10 15

aga ctg cca tac gtt gcc gac aag gac tcc atc tcc cag gag atc ttc 96
 Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
 20 25 30

gag aac aag atc atc acc gac gag acc aac gtt caa aac tac tcc gac 144
 Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
 35 40 45

aag ttc tct ttg gac gag tcc atc ctg gac ggt cag gtc cca atc aac 192
 Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
 50 55 60

cca gag atc gtc gac cca ctg ttg cca aac gtc aac atg gag cca ttg 240
 Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
 65 70 75 80

aac ttg cca ggt gag gag atc gtc ttc tac gac gac atc acc aag tac 288
 Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
 85 90 95

gtc gac tac ttg aac tcc tac tac tac ttg gag tct caa aag ttg tct 336
 Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
 100 105 110

aac aac gtc gag aac atc acc ttg acc acc tcc gtc gag gag gcc ttg 384
 Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
 115 120 125

ggt tac tct aac aag atc tac acc ttc ctg cca tcc ttg gct gag aag 432
 Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
 130 135 140

gtt aac aag ggt gtt caa gct ggt ttg ttc ctg aac tgg gcc aac gag 480
 Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
 145 150 155 160

gtc gtc gag gac ttc acc acc aac atc atg aag aag gac acc ctg gac 528
 Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
 165 170 175

aag atc tcc gac gtc tcc gtc atc atc cca tac atc ggt cca gcc ttg	576
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu	
180 185 190	
aac atc ggt aac tcc gcc ctg aga ggt aac ttc aac cag gcc ttc gcc	624
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala	
195 200 205	
acc gcc ggt gtc gcc ttc ctg ctg gag ggt ttc cca gag ttc acc atc	672
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile	
210 215 220	
cca gcc ctg ggt gtc ttc acc ttc tac tcc tcc atc cag gag aga gag	720
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu	
225 230 235 240	
aag atc atc aag acc atc gag aac tgc ttg gag cag aga gtc aag aga	768
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg	
245 250 255	
tgg aag gac tcc tac cag tgg atg gtt tcc aac tgg ctg tcc aga atc	816
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile	
260 265 270	
acc acc caa ttc aac cac atc aac tac cag atg tac gac tcc ctg tcc	864
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser	
275 280 285	
tac cag gcc gac gcc atc aag gcc aag atc gac ctg gag tac aag aag	912
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys	
290 295 300	
tac tcc ggt tcc gac aag gag aac atc aag tcc cag gtc gag aac ctg	960
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu	
305 310 315 320	
aag aac tcc ttg gac gtc aag atc tcc gag gcc atg aac aac atc aac	1008
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn	
325 330 335	
aag ttc atc cgt gag tgt tcc gtc acc tac ctg ttc aag aac atg ctg	1056
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu	
340 345 350	
cca aag gtc atc gac gag ctg aac aag ttc gac ctg aga acc aag acc	1104
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr	
355 360 365	
gag ctg atc aac ctg atc gac tcc cac aac atc atc ctg gtt ggt gag	1152
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu	
370 375 380	
gtt gac taa	1161
Val Asp	
385	

<210> 26
<211> 386
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTD Hn

<400> 26
Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
1 5 10 15
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
20 25 30
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
35 40 45
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
50 55 60
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
65 70 75 80
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
85 90 95
Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
100 105 110
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
115 120 125
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
130 135 140
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
145 150 155 160
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
165 170 175
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
180 185 190
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala
195 200 205
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile
210 215 220
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu
225 230 235 240
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg
245 250 255
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile
260 265 270
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser
275 280 285
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys
290 295 300
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu
305 310 315 320
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn
325 330 335
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu
340 345 350
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
355 360 365
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu

370
Val Asp
385

375

380

<210> 27
<211> 1149
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (1)...(1146)

<400> 27
atg tcc atc tgc atc gag atc aac aac ggt gag ctg ttc ttc gtg gct 48
Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
1 5 10 15

tcc gag aac agt tac aac gat gac aac atc aac act cct aag gag att 96
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
20 25 30

gac gac acc gtc act tct aac aac aac tac gaa aac gac ctg gac cag 144
Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
35 40 45

gtc atc cta aac ttc aac tcc gag tcc gcc cct ggt ctg tcc gac gag 192
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
50 55 60

aag ctg aac ctg acc atc cag aac gac gct tac atc cca aag tac gac 240
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
65 70 75 80

tcc aac ggt aca tcc gat atc gag cag cat gac gtt aac gag ctt aac 288
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
85 90 95

gtc ttc ttc tac tta gac gct cag aag gtg ccc gag ggt gag aac aac 336
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
100 105 110

gtc aat ctc acc tct tca att gac aca gcc ttg ttg gag cag cct aag 384
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys
115 120 125

atc tac acc ttc ttc tcc tcc gag ttc atc aac aac gtc aac aag cct 432
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro
130 135 140

gtg cag gcc gca ttg ttc gta agc tgg att cag cag gtg tta gta gac 480
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp
145 150 155 160

ttc act act gag gct aac cag aag tcc act gtt gac aag atc gct gac	528
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp	
165 170 175	
atc tcc atc gtc gtc cca tac atc ggt ctg gct ctg aac atc ggc aac	576
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn	
180 185 190	
gag gca cag aag ggc aac ttc aag gat gcc ctt gag ttg ttg ggt gcc	624
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala	
195 200 205	
ggt att ttg ttg gag ttc gaa ccc gag ctg ctg atc cct acc atc ctg	672
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu	
210 215 220	
gtc ttc acg atc aag tcc ttc ctg ggt tcc tcc gac aac aag aac aag	720
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys	
225 230 235 240	
gtc att aag gcc atc aac aac gcc ctg aag gag cgt gac gag aag tgg	768
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp	
245 250 255	
aag gaa gtc tat tcc ttc atc gtc tcg aac tgg atg acc aag atc aac	816
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn	
260 265 270	
acc cag ttc aac aag cga aag gag cag atg tac cag gct ctg cag aac	864
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn	
275 280 285	
cag gtc aac gcc atc aag acc atc atc gag tcc aag tac aac tcc tac	912
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr	
290 295 300	
acc ctg gag gag aag aac gag ctt acc aac aag tac gat atc aag cag	960
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln	
305 310 315 320	
atc gag aac gag ctg aac cag aag gtc tcc atc gcc atg aac aac atc	1008
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile	
325 330 335	
gac agg ttc ctg acc gag tcc tcc atc tcc tac ctg atg aag ctc atc	1056
Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile	
340 345 350	
aac gag gtc aag atc aac aag ctg cga gag tac gac gag aat gtc aag	1104
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys	
355 360 365	
acg tac ctg ctg aac tac atc atc cag cac gga tcc atc ctg	1146
Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu	
370 375 380	
taa	1149

Ca

<210> 28
<211> 382
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTE Hn

<400> 28

Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
1 5 10 15
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
20 25 30
Asp Asp Thr Val Thr Ser Asn Asn Tyr Glu Asn Asp Leu Asp Gln
35 40 45
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
50 55 60
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
65 70 75 80
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
85 90 95
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
100 105 110
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys
115 120 125
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro
130 135 140
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp
145 150 155 160
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp
165 170 175
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn
180 185 190
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala
195 200 205
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu
210 215 220
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys
225 230 235 240
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp
245 250 255
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn
260 265 270
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn
275 280 285
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr
290 295 300
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln
305 310 315 320
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile
325 330 335
Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile
340 345 350
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys
355 360 365

Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu
 370 375 380

<210> 29
 <211> 1227
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (1)...(1224)

<400> 29
 atg gcc cca cca cgt ctg tgt att aga gtc aac aac tca gaa tta ttc 48
 Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1 5 10 15

ttt gtc gct tcc gag tca agc tac aac gag aac gat att aac aca cct 96
 Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
 20 25 30

aaa gag att gac gat act acc aac cta aac aac aac tac cgg aac aac 144
 Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
 35 40 45

ttg gat gag gtt att ttg gat tac aac tca cag acc atc cct caa att 192
 Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
 50 55 60

tcc aac cgt acc tta aac act ctt gtc caa gac aac tcc tac gtt cca 240
 Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
 65 70 75 80

aga tac gat tct aac ggt acc tca gag atc gag gag tat gat gtt gtt 288
 Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
 85 90 95

gac ttt aac gtc ttt ttc tat ttg cat gcc cag aag gtg cca gaa ggt 336
 Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
 100 105 110

gaa acc aac atc tca ttg act tct tcc att gat acc gcc ttg ttg gaa 384
 Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu
 115 120 125

gag tcc aag gat atc ttc ttt tct tcg gag ttt atc gat act atc aac 432
 Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn
 130 135 140

aag cct gtc aac gcc gct ctg ttc att gat tgg att agc aag gtc atc 480
 Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile
 145 150 155 160

aga gat ttt acc act gaa gct act caa aag tcc act gtt gat aag att 528

Arg	Asp	Phe	Thr	Thr	Glu	Ala	Thr	Gln	Lys	Ser	Thr	Val	Asp	Lys	Ile	
				165					170					175		
gct	gac	atc	tct	ttg	att	gtc	ccc	tat	gtc	ggc	ctt	gct	ttg	aac	atc	576
Ala	Asp	Ile	Ser	Leu	Ile	Val	Pro	Tyr	Val	Gly	Leu	Ala	Leu	Asn	Ile	
			180					185					190			
att	att	gag	gca	gaa	aag	ggc	aac	ttt	gag	gag	gct	ttt	gaa	ttg	ttg	624
Ile	Ile	Glu	Ala	Glu	Lys	Gly	Asn	Phe	Glu	Glu	Ala	Phe	Glu	Leu	Leu	
		195					200					205				
gga	gtt	ggc	att	ttg	ttg	gag	ttt	gtt	cca	gaa	ctt	acc	att	cct	gtc	672
Gly	Val	Gly	Ile	Leu	Leu	Glu	Phe	Val	Pro	Glu	Leu	Thr	Ile	Pro	Val	
	210					215					220					
att	tta	gtt	ttt	acg	atc	aag	tcc	tac	atc	gat	tca	tac	gag	aac	aag	720
Ile	Leu	Val	Phe	Thr	Ile	Lys	Ser	Tyr	Ile	Asp	Ser	Tyr	Glu	Asn	Lys	
225					230					235					240	
aat	aaa	gca	att	aaa	gct	att	aac	aac	tcc	ttg	atc	gaa	aga	gag	gct	768
Asn	Lys	Ala	Ile	Lys	Ala	Ile	Asn	Asn	Ser	Leu	Ile	Glu	Arg	Glu	Ala	
				245					250					255		
aag	tgg	aag	gaa	atc	tac	tca	tgg	att	gta	tca	aac	tgg	ctt	act	aga	816
Lys	Trp	Lys	Glu	Ile	Tyr	Ser	Trp	Ile	Val	Ser	Asn	Trp	Leu	Thr	Arg	
			260					265					270			
att	aac	act	caa	ttt	aac	aag	aga	aag	gag	caa	atg	tac	cag	gct	ctg	864
Ile	Asn	Thr	Gln	Phe	Asn	Lys	Arg	Lys	Glu	Gln	Met	Tyr	Gln	Ala	Leu	
		275					280					285				
caa	aac	caa	gtc	gat	gct	atc	aag	act	gca	att	gaa	tac	aag	tac	aac	912
Gln	Asn	Gln	Val	Asp	Ala	Ile	Lys	Thr	Ala	Ile	Glu	Tyr	Lys	Tyr	Asn	
	290					295					300					
aac	tat	act	tcc	gat	gag	aag	aac	aga	ctt	gaa	tct	gaa	tac	aat	atc	960
Asn	Tyr	Thr	Ser	Asp	Glu	Lys	Asn	Arg	Leu	Glu	Ser	Glu	Tyr	Asn	Ile	
305					310					315					320	
aac	aac	att	gaa	gaa	gag	ttg	aac	aag	aaa	gtt	tct	ttg	gct	atg	aag	1008
Asn	Asn	Ile	Glu	Glu	Glu	Leu	Asn	Lys	Lys	Val	Ser	Leu	Ala	Met	Lys	
			325						330					335		
aat	atc	gaa	aga	ttt	atg	acc	gaa	tcc	tct	atc	tct	tac	ttg	atg	aag	1056
Asn	Ile	Glu	Arg	Phe	Met	Thr	Glu	Ser	Ser	Ile	Ser	Tyr	Leu	Met	Lys	
			340					345					350			
ttg	atc	aat	gag	gcc	aag	gtt	ggc	aag	ttg	aag	aag	tac	gat	aac	cac	1104
Leu	Ile	Asn	Glu	Ala	Lys	Val	Gly	Lys	Leu	Lys	Lys	Tyr	Asp	Asn	His	
		355					360					365				
gtt	aag	agc	gat	ctg	ctg	aac	tac	att	ctc	gac	cac	aga	tca	atc	ctg	1152
Val	Lys	Ser	Asp	Leu	Leu	Asn	Tyr	Ile	Leu	Asp	His	Arg	Ser	Ile	Leu	
	370					375					380					
gga	gag	cag	aca	aac	gag	ctg	agt	gat	ttg	gtt	act	tcc	act	ttg	aac	1200
Gly	Glu	Gln	Thr	Asn	Glu	Leu	Ser	Asp	Leu	Val	Thr	Ser	Thr	Leu	Asn	

385

390

395

400

tcc tcc att cca ttt gag ctt tct taa

1227

Ser Ser Ile Pro Phe Glu Leu Ser

405

<210> 30

<211> 408

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTF Hn

<400> 30

Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1 5 10 15
 Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
 20 25 30
 Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
 35 40 45
 Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
 50 55 60
 Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
 65 70 75 80
 Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
 85 90 95
 Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
 100 105 110
 Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu
 115 120 125
 Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn
 130 135 140
 Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile
 145 150 155 160
 Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys Ser Thr Val Asp Lys Ile
 165 170 175
 Ala Asp Ile Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile
 180 185 190
 Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu Glu Ala Phe Glu Leu Leu
 195 200 205
 Gly Val Gly Ile Leu Leu Glu Phe Val Pro Glu Leu Thr Ile Pro Val
 210 215 220
 Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile Asp Ser Tyr Glu Asn Lys
 225 230 235 240
 Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser Leu Ile Glu Arg Glu Ala
 245 250 255
 Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg
 260 265 270
 Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu
 275 280 285
 Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn
 290 295 300
 Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile
 305 310 315 320

Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys
 325 330 335
 Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys
 340 345 350
 Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Lys Tyr Asp Asn His
 355 360 365
 Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu
 370 375 380
 Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn
 385 390 395 400
 Ser Ser Ile Pro Phe Glu Leu Ser
 405

<210> 31

<211> 1233

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hc

<221> CDS

<222> (1) ... (1230)

<400> 31

atg gcc aaa aat acc ggt aaa tct gaa cag tgt att att gtt aat aat 48
 Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
 1 5 10 15

 gag gat tta ttt ttc ata gct aat aaa gat agt ttt tca aaa gat tta 96
 Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
 20 25 30

 gct aaa gca gaa act ata gca tat aat aca caa aat aat act ata gaa 144
 Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
 35 40 45

 aat aat ttt tct ata gat cag ttg att tta gat aat gat tta agc agt 192
 Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
 50 55 60

 ggc ata gac tta cca aat gaa aac aca gaa cca ttt aca aat ttt gac 240
 Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
 65 70 75 80

 gac ata gat atc cct gtg tat att aaa caa tct gct tta aaa aaa att 288
 Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
 85 90 95

 ttt gtg gat gga gat agc ctt ttt gaa tat tta cat gct caa aca ttt 336
 Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
 100 105 110

 cct tct aat ata gaa aat cta caa cta acg aat tca tta aat gat gct 384
 Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
 115 120 125

tta	aga	aat	aat	aat	aaa	gtc	tat	act	ttt	ttt	tct	aca	aac	ctt	gtt	432
Leu	Arg	Asn	Asn	Asn	Lys	Val	Tyr	Thr	Phe	Phe	Ser	Thr	Asn	Leu	Val	
	130					135					140					

gaa	aaa	gct	aat	aca	gtt	gta	ggg	gct	tca	ctt	ttt	gta	aac	tg	gta	480
Glu	Lys	Ala	Asn	Thr	Val	Val	Gly	Ala	Ser	Leu	Phe	Val	Asn	Trp	Val	
145					150					155					160	

aaa	gga	gta	ata	gat	gat	ttt	aca	tct	gaa	tcc	aca	caa	aaa	agt	act	528
Lys	Gly	Val	Ile	Asp	Asp	Phe	Thr	Ser	Glu	Ser	Thr	Gln	Lys	Ser	Thr	
				165					170					175		

ata	gat	aaa	gtt	tca	gat	gta	tcc	ata	att	att	ccc	tat	ata	gga	cct	576
Ile	Asp	Lys	Val	Ser	Asp	Val	Ser	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	
			180					185					190			

gct	ttg	aat	gta	gga	aat	gaa	aca	gct	aaa	gaa	aat	ttt	aaa	aat	gct	624
Ala	Leu	Asn	Val	Gly	Asn	Glu	Thr	Ala	Lys	Glu	Asn	Phe	Lys	Asn	Ala	
	195					200						205				

ttt	gaa	ata	ggg	gga	gcc	gct	atc	tta	atg	gag	ttt	att	cca	gaa	ctt	672
Phe	Glu	Ile	Gly	Gly	Ala	Ala	Ile	Leu	Met	Glu	Phe	Ile	Pro	Glu	Leu	
	210					215					220					

att	gta	cct	ata	gtt	gga	ttt	ttt	aca	tta	gaa	tca	tat	gta	gga	aat	720
Ile	Val	Pro	Ile	Val	Gly	Phe	Phe	Thr	Leu	Glu	Ser	Tyr	Val	Gly	Asn	
225					230					235					240	

aaa	ggg	cat	att	att	atg	acg	ata	tcc	aat	gct	tta	aag	aaa	agg	gat	768
Lys	Gly	His	Ile	Ile	Met	Thr	Ile	Ser	Asn	Ala	Leu	Lys	Lys	Arg	Asp	
				245					250					255		

caa	aaa	tg	aca	gat	atg	tat	ggg	ttg	ata	gta	tcg	cag	tg	ctc	tca	816
Gln	Lys	Trp	Thr	Asp	Met	Tyr	Gly	Leu	Ile	Val	Ser	Gln	Trp	Leu	Ser	
			260					265					270			

acg	gtt	aat	act	caa	ttt	tat	aca	ata	aaa	gaa	aga	atg	tac	aat	gct	864
Thr	Val	Asn	Thr	Gln	Phe	Tyr	Thr	Ile	Lys	Glu	Arg	Met	Tyr	Asn	Ala	
		275					280					285				

tta	aat	aat	caa	tca	caa	gca	ata	gaa	aaa	ata	ata	gaa	gat	caa	tat	912
Leu	Asn	Asn	Gln	Ser	Gln	Ala	Ile	Glu	Lys	Ile	Ile	Glu	Asp	Gln	Tyr	
	290					295					300					

aat	aga	tat	agt	gaa	gaa	gat	aaa	atg	aat	att	aac	att	gat	ttt	aat	960
Asn	Arg	Tyr	Ser	Glu	Glu	Asp	Lys	Met	Asn	Ile	Asn	Ile	Asp	Phe	Asn	
305					310					315				320		

gat	ata	gat	ttt	aaa	ctt	aat	caa	agt	ata	aat	tta	gca	ata	aac	aat	1008
Asp	Ile	Asp	Phe	Lys	Leu	Asn	Gln	Ser	Ile	Asn	Leu	Ala	Ile	Asn	Asn	
				325					330					335		

ata	gat	gat	ttt	ata	aac	caa	tgt	tct	ata	tca	tat	cta	atg	aat	aga	1056
Ile	Asp	Asp	Phe	Ile	Asn	Gln	Cys	Ser	Ile	Ser	Tyr	Leu	Met	Asn	Arg	
			340					345					350			

atg att cca tta gct gta aaa aag tta aaa gac ttt gat gat aat ctt 1104
Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu
355 360 365

aag aga gat tta ttg gag tat ata gat aca aat gaa cta tat tta ctt 1152
Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu
370 375 380

gat gaa gta aat att cta aaa tca aaa gta aat aga cac cta aaa gac 1200
Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp
385 390 395 400

agt ata cca ttt gat ctt tca cta tat acc taa 1233
Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr
405 410

<210> 32
<211> 410
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTG Hn

cg
<400> 32
Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
1 5 10 15
Glu Asp Leu Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
20 25 30
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
35 40 45
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
50 55 60
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
65 70 75 80
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
85 90 95
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
100 105 110
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
115 120 125
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
130 135 140
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val
145 150 155 160
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr
165 170 175
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro
180 185 190
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala
195 200 205
Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu
210 215 220
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn
225 230 235 240

Ile	Ile	Tyr	Asn	Gly	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val		
	80						85				90						
cgt	atc	ccg	aaa	tac	ttc	aac	aaa	gtt	aac	ctg	aac	aac	gaa	tac	act	339	
Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr	Thr		
	95				100				105						110		
atc	atc	gac	tgc	atc	cgt	aac	aac	aac	tct	ggg	tgg	aaa	atc	tct	ctg	387	
Ile	Ile	Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu		
				115					120					125			
aac	tac	aac	aaa	atc	atc	tgg	act	ctg	cag	gac	act	gct	ggg	aac	aac	435	
Asn	Tyr	Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn		
			130					135					140				
cag	aaa	ctg	gtt	ttc	aac	tac	act	cag	atg	atc	tct	atc	tct	gac	tac	483	
Gln	Lys	Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr		
		145					150					155					
att	aac	aaa	tgg	atc	ttc	gtt	act	atc	act	aac	aac	cgt	ctg	ggg	aac	531	
Ile	Asn	Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn		
	160					165					170						
tct	cgt	atc	tac	atc	aac	ggg	aac	ctg	atc	gat	gaa	aaa	tct	atc	tct	579	
Ser	Arg	Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser		
	175				180					185					190		
aac	ctg	ggg	gac	atc	cac	gtt	tct	gac	aac	atc	ctg	ttc	aaa	atc	gtt	627	
Asn	Leu	Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val		
				195				200						205			
ggg	tgc	aac	gac	acg	cgt	tac	gtt	ggg	atc	cgt	tac	ttc	aaa	gtt	ttc	675	
Gly	Cys	Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe		
			210					215					220				
gac	act	gaa	ctg	ggg	aaa	act	gaa	atc	gaa	act	ctg	tac	tct	gac	gaa	723	
Asp	Thr	Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu		
		225					230					235					
ccg	gac	ccg	tct	atc	ctg	aaa	gac	ttc	tgg	ggg	aac	tac	ctg	ctg	tac	771	
Pro	Asp	Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr		
	240					245					250						
aac	aaa	cgt	tac	tac	ctg	ctg	aac	ctg	ctc	cgg	act	gac	aaa	tct	atc	819	
Asn	Lys	Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile		
	255				260					265					270		
act	cag	aac	tct	aac	ttc	ctg	aac	atc	aac	cag	cag	cgt	ggg	gtt	tat	867	
Thr	Gln	Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr		
				275					280					285			
cag	aaa	cct	aac	atc	ttc	tct	aac	act	cgt	ctg	tac	act	ggg	gtt	gaa	915	
Gln	Lys	Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu		
			290					295					300				
gtt	atc	atc	cgt	aaa	aac	ggg	tct	act	gac	atc	tct	aac	act	gac	aac	963	
Val	Ile	Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn		

305	310	315	
ttc gta cgt aaa aac gac ctg gct tac atc aac gtt gtt gac cgt gac			1011
Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp			
320	325	330	
gtt gaa tac cgt ctg tac gct gac atc tct atc gct aaa ccg gaa aaa			1059
Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys			
335	340	345	350
atc atc aaa ctg atc cgt act tct aac tct aac aac tct ctg ggt cag			1107
Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln			
	355	360	365
atc atc gtt atg gac tcg atc ggt aac aac tgc act atg aac ttc cag			1155
Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln			
	370	375	380
aac aac aac ggt ggt aac atc ggt ctg ctg ggt ttc cac tct aac aac			1203
Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn			
	385	390	395
ctg gtt gct tct tca tgg tac tac aac aac atc cgt aaa aac act tct			1251
Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser			
	400	405	410
tct aac ggt tgc ttc tgg tct ttc atc tct aaa gaa cac ggt tgg cag			1299
Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln			
	415	420	425
			430
gaa aac taagaattc			1314
Glu Asn			

<210> 34

<211> 432

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTF Hc

<400> 34

Met	Ser	Tyr	Thr	Asn	Asp	Lys	Ile	Leu	Ile	Leu	Tyr	Phe	Asn	Lys	Leu
1				5				10					15		
Tyr	Lys	Lys	Ile	Lys	Asp	Asn	Ser	Ile	Leu	Asp	Met	Arg	Tyr	Glu	Asn
			20					25				30			
Asn	Lys	Phe	Ile	Asp	Ile	Ser	Gly	Tyr	Gly	Ser	Asn	Ile	Ser	Ile	Asn
		35					40				45				
Gly	Asp	Val	Tyr	Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe	Gly	Ile	Tyr
	50					55				60					
Ser	Ser	Lys	Pro	Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn	Asp	Ile	Ile
65					70				75					80	
Tyr	Asn	Gly	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val	Arg	Ile
				85					90					95	

Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
 100 105 110
 Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
 115 120 125
 Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
 130 135 140
 Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
 145 150 155 160
 Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
 165 170 175
 Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
 180 185 190
 Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
 195 200 205
 Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
 210 215 220
 Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
 225 230 235 240
 Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
 245 250 255
 Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
 260 265 270
 Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
 275 280 285
 Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
 290 295 300
 Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
 305 310 315 320
 Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
 325 330 335
 Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
 340 345 350
 Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
 355 360 365
 Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
 370 375 380
 Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
 385 390 395 400
 Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn
 405 410 415
 Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
 420 425 430

<210> 35
 <211> 1278
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (10)...(1269)

<400> 35
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Met Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile
 1 5 10

aag tct tct tcc gtt tta aac atg aga tac aag aat gat aaa tac gtc 99
 Lys Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val
 15 20 25 30

gac act tcc ggt tac gac tcc aat atc aac att aac ggt gac gtg tac 147
 Asp Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr
 35 40 45

aag tac cca act aac aaa aac caa ttc ggt atc tac aac gac aag ctt 195
 Lys Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu
 50 55 60

act gag ctg aac atc tct caa aac gac tac att atc tac gac aac aag 243
 Thr Glu Leu Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys
 65 70 75

tac aat aac ttc tct att tct ttc tgg gtc aga att cct aac tac gat 291
 Tyr Asn Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp
 80 85 90

aac aag atc gtc aac gtt aac aac gag tac act atc atc aac tgt atg 339
 Asn Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
 95 100 105 110

aga gac aac aac tcc ggt tgg aag gtc tct ctt aac cac aac gag atg 387
 Arg Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Met
 115 120 125

att tgg acc ttg caa gac aac gca ggt att aac caa aag tta gca ttc 435
 Ile Trp Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe
 130 135 140

aac tac ggt aac gca aac ggt att tct gac tac atc aac aag tgg att 483
 Asn Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile
 145 150 155

ttc gtc act atc act aac gac aga tta ggg gac tct aag ctt tac att 531
 Phe Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile
 160 165 170

aac ggt aac tta atc gac caa aag tcc att tta aac tta ggt aac att 579
 Asn Gly Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile
 175 180 185 190

cac gtt tct gac aac atc tta ttc aag atc gtt aac tgc agt tac aac 627
 His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Asn
 195 200 205

aga tac att ggc att aga tac ttc aac att ttc gac aag gag tta gac 675
 Arg Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp
 210 215 220

gag acc gag att caa act tta tac agc aac gaa cct aac acc aat att 723
 Glu Thr Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile

225	230	235	
tta tta aac gtg tta aag cca aac aac ttc att gat agg aga aag gat			771
Leu Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp			
255	260	265	270
tct act tta agc att aac aac atc aga agc act att ctt tta gct aac			819
Ser Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn			
275	280	285	
aga tta tac tct ggt atc aag gtt aag atc caa aga gtt aac aac tct			915
Arg Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser			
290	295	300	
tct act aac gat aac ctt gtt aga aag aac gat cag gtc tat att aac			963
Ser Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn			
305	310	315	
ttc gtc gct agc aag act cac tta ttc cca tta tat gct gat aac gct			1011
Phe Val Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Asn Ala			
320	325	330	
acc acc aac aag gag aag acc atc aag atc tcc tcc tct ggc aac aga			1059
Thr Thr Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg			
335	340	345	350
ttt aac caa gtc gtc gtt atg aac tcc gtc ggt aac aac tgt acc atg			1107
Phe Asn Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met			
355	360	365	
aac ttt aaa aat aat aat gga aat aat att ggg tgt tta ggt ttc aag			1155
Asn Phe Lys Asn Asn Asn Gly Asn Asn Ile Gly Cys Leu Gly Phe Lys			
370	375	380	
gca gat act gta gtt gct agt act tgg tat tat acc cac atg aga gat			1203
Ala Asp Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp			
385	390	395	
cac acc aac agc aat gga tgt ttt tgg aac ttt att tct gaa gaa cat			1251
His Thr Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His			
400	405	410	
gga tgg caa gaa aaa taa tagggatcc			1278
Gly Trp Gln Glu Lys *			
415			

<210> 36

<211> 419

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BONTÉ Hc

<400> 36

Met Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser
1 5 10 15
Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr
20 25 30
Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr
35 40 45
Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu
50 55 60
Leu Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys
65 70 75 80
Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys
85 90 95
Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp
100 105 110
Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp
115 120 125
Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr
130 135 140
Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val
145 150 155 160
Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly
165 170 175
Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val
180 185 190
Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr
195 200 205
Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr
210 215 220
Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys
225 230 235 240
Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu
245 250 255
Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr
260 265 270
Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu
275 280 285
Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr
290 295 300
Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val
305 310 315 320
Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr
325 330 335
Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn
340 345 350
Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe
355 360 365
Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp
370 375 380
Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr
385 390 395 400
Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp
405 410 415
Gln Glu Lys

<210> 37
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (9)...(1325)

<400> 37

ctcgagcc atg gct cgt ctg ctg tct acc ttc act gaa tac atc aag aac 50
Met Ala Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn
1 5 10

atc atc aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg 98
Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu
15 20 25 30

atc gac ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt 146
Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val
35 40 45

aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa 194
Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu
50 55 60

tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct 242
Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser
65 70 75

atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac 290
Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr
80 85 90

ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg 338
Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
95 100 105 110

gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc 386
Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile
115 120 125

tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa 434
Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys
130 135 140

tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc 482
Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe
145 150 155

ggt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac 530
Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn

160	165	170	
ggc cgt ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His 175 180 185 190			578
gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His 195 200 205			626
cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn 210 215 220			674
gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile 225 230 235			722
ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr 240 245 250			770
atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val 255 260 265 270			818
ggg atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met 275 280 285			866
act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe 290 295 300			914
atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn 305 310 315			962
aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg 320 325 330			1010
ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala 335 340 345 350			1058
ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys 355 360 365			1106
tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln 370 375 380			1154
gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn 385 390 395			1202

aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa 1250
 Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu
 400 405 410

cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat 1298
 Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp
 415 420 425 430

gac ggt tgg ggt gaa cgt ccg ctg taa cccgggaaag ctt 1338
 Asp Gly Trp Gly Glu Arg Pro Leu *
 435

<210> 38
 <211> 415
 <212> PRT
 <213> Clostridium botulinum

Ca <400> 38
 Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys
 1 5 10 15
 Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln
 20 25 30
 Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys
 35 40 45
 Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
 50 55 60
 Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu
 65 70 75 80
 Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser
 85 90 95
 Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile
 100 105 110
 Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp
 115 120 125
 Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn
 130 135 140
 Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile
 145 150 155 160
 Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu
 165 170 175
 Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Phe Tyr Phe Asn
 180 185 190
 Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp
 195 200 205
 Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu
 210 215 220
 Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys
 225 230 235 240
 Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys
 245 250 255
 Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser
 260 265 270
 Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn
 275 280 285
 Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val

290 295 300
 Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly
 305 310 315 320
 Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu
 325 330 335
 Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn
 340 345 350
 Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe
 355 360 365
 Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn
 370 375 380
 Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser
 385 390 395 400
 Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
 405 410 415

<210> 39
 <211> 1348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTB Hc
 <221> CDS
 <222> (1)...(1323)

<400> 39
 atg gcc aac aaa tac aat tcc gaa atc ctg aac aat atc atc ctg aac 48
 Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn
 1 5 10 15

 ctg cgt tac aaa gac aac aat ctg atc gat ctg tct ggt tac ggt gct 96
 Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala
 20 25 30

 aaa gtt gaa gta tac gac ggt gtt gaa ctg aat gac aag aac cag ttc 144
 Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe
 35 40 45

 aaa ctg acc tct tcc gct aac tct aag atc cgt gtt act cag aat cag 192
 Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln
 50 55 60

 aac atc atc ttc aac tcc gta ttc ctg gac ttc tct gtt tcc ttc tgg 240
 Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp
 65 70 75 80

 atc cgt atc ccg aaa tac aag aac gac ggt atc cag aat tac atc cac 288
 Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His
 85 90 95

 aat gaa tac acc atc atc aac tgc atg aag aat aac tct ggt tgg aag 336
 Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys
 100 105 110

atc tcc atc cgc ggt aac cgt atc atc tgg act ctg atc gat atc aac 384
 Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn
 115 120 125

ggt aag acc aaa tct gta ttc ttc gaa tac aac atc cgt gaa gac atc 432
 Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile
 130 135 140

tct gaa tac atc aat cgc tgg ttc ttc gtt acc atc acc aat aac ctg 480
 Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu
 145 150 155 160

aac aat gct aaa atc tac atc aac ggt aaa ctg gaa tct aat acc gac 528
 Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp
 165 170 175

atc aaa gac atc cgt gaa gtt atc gct aac ggt gaa atc atc ttc aaa 576
 Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys
 180 185 190

ctg gac ggt gac atc gat cgt acc cag ttc atc tgg atg aaa tac ttc 624
 Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe
 195 200 205

tcc atc ttc aac acc gaa ctg tct cag tcc aat atc gaa gaa cgg tac 672
 Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr
 210 215 220

aag atc cag tct tac tcc gaa tac ctg aaa gac ttc tgg ggt aat ccg 720
 Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro
 225 230 235 240

ctg atg tac aac aaa gaa tac tat atg ttc aat gct ggt aac aag aac 768
 Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn
 245 250 255

tct tac atc aaa ctg aag aaa gac tct ccg gtt ggt gaa atc ctg act 816
 Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr
 260 265 270

cgt tcc aaa tac aac cag aac tct aaa tac atc aac tac cgc gac ctg 864
 Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu
 275 280 285

tac atc ggt gaa aag ttc atc atc cgt cgc aaa tct aac tct cag tcc 912
 Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser
 290 295 300

atc aat gat gac atc gta cgt aaa gaa gac tac atc tac ctg gac ttc 960
 Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe
 305 310 315 320

ttc aac ctg aat cag gaa tgg cgt gta tac acc tac aag tac ttc aag 1008
 Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys
 325 330 335

aaa gaa gaa gaa aag ctt ttc ctg gct ccg atc tct gat tcc gac gaa 1056

Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu
 340 345 350

ctc tac aac acc atc cag atc aaa gaa tac gac gaa cag ccg acc tac 1104
 Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr
 355 360 365

tct tgc cag ctg ctg ttc aag aaa gat gaa gaa tct act gac gaa atc 1152
 Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile
 370 375 380

ggc ctg atc ggc atc cac cgt ttc tac gaa tct ggc atc gta ttc gaa 1200
 Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu
 385 390 395 400

gaa tac aaa gac tac ttc tgc atc tcc aaa tgg tac ctg aag gaa gtt 1248
 Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val
 405 410 415

aaa cgc aaa ccg tac aac ctg aaa ctg ggc tgc aat tgg cag ttc atc 1296
 Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile
 420 425 430

ccg aaa gac gaa ggc tgg acc gaa tag taacctctag agtcgaggcc 1343
 Pro Lys Asp Glu Gly Trp Thr Glu *
 435 440

tgacag 1348

<210> 40

<211> 436

<212> PRT

<213> Clostridium botulinum

<400> 40

Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn Leu
 1 5 10 15
 Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala Lys
 20 25 30
 Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe Lys
 35 40 45
 Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln Asn
 50 55 60
 Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp Ile
 65 70 75 80
 Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His Asn
 85 90 95
 Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys Ile
 100 105 110
 Ser Ile Arg Gly Asn Arg Ile Trp Thr Leu Ile Asp Ile Asn Gly Lys
 115 120 125
 Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile Ser Glu
 130 135 140
 Tyr Ile Asn Arg Trp Phe Val Thr Ile Thr Asn Asn Leu Asn Asn
 145 150 155 160
 Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp Ile Lys
 165 170 175

Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys Leu Asp
 180 185 190
 Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe Ser Ile
 195 200 205
 Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr Lys Ile
 210 215 220
 Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro Leu Met
 225 230 235 240
 Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser Tyr
 245 250 255
 Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr Arg Ser
 260 265 270
 Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu Tyr Ile
 275 280 285
 Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser Ile Asn
 290 295 300
 Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe Phe Asn
 305 310 315 320
 Leu Asn Gln Glu Arg Val Tyr Thr Tyr Lys Phe Lys Lys Glu Glu Glu
 325 330 335
 Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu Phe Tyr Asn Thr
 340 345 350
 Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr Ser Cys Gln Leu
 355 360 365
 Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile Gly Leu Ile Gly
 370 375 380
 Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu Glu Tyr Lys Asp
 385 390 395 400
 Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val Lys Arg Lys Pro
 405 410 415
 Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro Lys Asp Glu
 420 425 430
 Gly Trp Thr Glu
 435

<210> 41
 <211> 848
 <212> PRT
 <213> Clostridium botulinum

<400> 41
 Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
 1 5 10 15
 Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
 20 25 30
 Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
 35 40 45
 Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
 50 55 60
 Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
 65 70 75 80
 Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
 85 90 95
 Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
 100 105 110
 His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu

115 120 125
 Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
 130 135 140
 Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu
 145 150 155 160
 Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
 165 170 175
 Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
 180 185 190
 Leu Asn Ile Gly Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu Ile
 195 200 205
 Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala Ile
 210 215 220
 Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val
 225 230 235 240
 Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu Lys
 245 250 255
 Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val
 260 265 270
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 Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn Gln
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 Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu
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 Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile Asn
 325 330 335
 Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile
 340 345 350
 Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys Asp
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 Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile Gly Gln
 370 375 380
 Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp Ile
 385 390 395 400
 Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser Thr
 405 410 415
 Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu
 420 425 430
 Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys
 435 440 445
 Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln
 450 455 460
 Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys
 465 470 475 480
 Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
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 Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu
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 Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser
 515 520 525
 Leu Asn Tyr Gly Glu Ile Ile Thr Thr Leu Gln Asp Thr Gln Glu Ile
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 Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp
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 Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn
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Asn Ser Lys Ile Tyr Thr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
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 Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys
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 Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe
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 Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr
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 Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr
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 Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Ile Leu Leu Tyr Asp Pro Asn
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 Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu
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 Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser
 690 695 700
 Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
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 Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
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 Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
 740 745 750
 Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
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 Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr
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 Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
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 Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile Asn
 35 40 45
 Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro Ser
 50 55 60
 Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val Tyr
 65 70 75 80
 Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr Ile
 85 90 95
 Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp Ile
 100 105 110
 Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys Val

115 120 125
 Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val Val
 130 135 140
 Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp Phe
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 Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp Ile
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 Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn Glu
 180 185 190
 Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala Ser
 195 200 205
 Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly Ala
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 Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys Thr
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 Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met Tyr
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 Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe Tyr
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 Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln Ala
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 Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys Glu
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 Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val Glu
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 385 390 395 400
 Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe Asn Lys Tyr Asn
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 Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn Leu Arg Tyr Lys Asp Asn
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 Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala Lys Val Glu Val Tyr Asp
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 Gly Val Glu Leu Asn Asp Lys Asn Gln Phe Lys Leu Thr Ser Ser Ala
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 Asn Ser Lys Ile Arg Thr Gln Asn Gln Asn Ile Ile Phe Asn Ser Val
 465 470 475 480
 Phe Leu Asp Phe Ser Val Ser Phe Trp Ile Arg Ile Pro Lys Tyr Lys
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 Asn Asp Gly Ile Gln Asn Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn
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 Cys Met Lys Asn Asn Ser Gly Trp Lys Ile Ser Ile Arg Gly Arg Ile
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 Ile Trp Thr Leu Ile Asp Ile Asn Gly Lys Thr Lys Ser Val Phe Phe
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 Phe Val Thr Ile Thr Asn Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn
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Gly Lys Leu Glu Ser Asn Thr Asp Ile Lys Asp Ile Arg Glu Val Ile
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 Gln Phe Ile Trp Met Lys Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser
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